



MATCH WITH FIG. 1A

241	AAGCTATTCTCTTTCACCAAGTACTTTCTCAAGATTGAGAAGAACGGGAAGGTCAGCGGG	300
	-----+-----+-----+-----+-----+-----+-----+	
	TTCGATAAGAGAAAAGTGGTTCATGAAAGAGTTCTAACTCTTCTTGCCCTTCCAGTCGCCC	
	K L F S F T K Y F L K I E K N G K V S G	
301	ACCAAGAAGGAGAACTGCCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTT	360
	-----+-----+-----+-----+-----+-----+-----+	
	TGGTTCTTCCTCTTGACGGGCATGTCGTAGGACCTCTATTGTAGTCATCTTTAGCCTCAA	
	T K K E N C P Y S I L E I T S V E I G V	
361	GTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAACTC	420
	-----+-----+-----+-----+-----+-----+-----+	
	CAACGGCAGTTTCGGTAATTGTCGTTGATAATGAATCGGTACTTGTTCTTCCCCTTTGAG	
	V A V K A I N S N Y Y L A M N K K G K L	
421	TATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGA	480
	-----+-----+-----+-----+-----+-----+-----+	
	ATACCGAGTTTTCTTAAATTGTTACTGACATTCGACTTCCTCTCCTATCTCCTTTTACCT	
	Y G S K E F N N D C K L K E R I E E N G	

MATCH WITH FIG. 1C

FIG.1B

MATCH WITH FIG. 1B

204070" at 900F

```

      TACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTG
481  -----+-----+-----+-----+-----+-----+ 540
      ATGTTATGGATACGTAGTAAATTGACCGTCGTATTACCCTCCGTTTACATACACCGTAAC

      Y N T Y A S F N W Q H N G R Q M Y V A L

      AATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCAC
541  -----+-----+-----+-----+-----+-----+ 600
      TTACCTTTTCCTCGAGGTTCTCTCCTGTCTTTTGTGCTTCCTTTTGTGGAGACGAGTG

      N G K G A P R R G Q K T R R K N T S A H

      TTTCTTCCAATGGTGGTACACTCATAG
601  -----+-----+----- 627
      AAAGAAGGTTACCACCATGTGAGTATC

      F L P M V V H S *
```

FIG.1C

	1		50
FGF4	MS.GPGTAAV ALLPAVLLAL LA.....	.PWAGRGGAA APTAPNGTLE	
FGF6	MSRGAGRLQG TLWALVFLGI LV.....	.GMVVPSPAG TR.ANNTLLD	
FGF5	.....MSL SFLLLLFFSH LILSAWAHGE	KRLAPKGQPG PAATDRNPIG	
FGF1	.....	.....	
FGF2	.....	.....	
FGF9	.....	..MAPLGEVG NYFGVQDAVP	
FGF7	.....MHKW ILTWILPTLL .....	YRSCF HIICLVGTIS	
KGF2	.....MWKW ILTHCASAFP HLPGCCCCCF	LLLFLVSSVP	
FGF3	.....	.....MGL IWLLLLSLLE	
FGF8	MGSPRSALSC LLLHLLVLCL QAQVRSAAQK	RGPGAGNPAD TLGQGHEDRP	

	51		100
FGF4	AELERRWESL VALSLARLPV AA..QPKEAA	VQSGAGDY.. ...LLGIKRL	
FGF6	S...RGWGTL LSRSRAGLAG EI.....AG	VNWESG.Y.. ...LVGIKRQ	
FGF5	SSSRQSSSSA MSSSSASSSP AASLGSQGSG	LEQSSFQW.. ...SPSGRRT	
FGF1	.....MAEG EITTFTALTE KFN...LPPG	.....N.. ...YK...KP	
FGF2	.....MAAG SITTLPALPE DGGSGAFPPG	.....H.. ...FK...DP	
FGF9	FGNVPVLPVD SPVLLSDHLG QSEAGGLPRG	PAVTDLDH.. ...LKGILRR	
FGF7	LACNDMTPEQ M...ATNVNC .....	SSPE RHTRSYDY.. ...MEGGDIR	
KGF2	VTCQALGQDM VSPEATNSSS SSFSSPSSAG	RHVRSYNH.. ...LQ.GDVR	
FGF3	PGWPAAGPGA .....	...RLRRDAG GRGGVYEH.. ...L.GGAPR	
FGF8	FGQRSRAGKN FTNPAPNYPE EGSKEQRDSV	LPKVTQRHVR EQSLVTDQLS	

MATCH WITH FIG. 2B

FIG.2A

MATCH WITH FIG. 2A

	101		150
FGF4	RRL.....YC NVGIGFHLQA	LPDGRIGGAH	ADT.RDSLLE LSPVERGV.V
FGF6	RRL.....YC NVGIGFHLQV	LPDGRISGTH	EEN.PYSLLE ISTVERGV.V
FGF5	GSL.....YC RVGIGFHLQI	YPDGVNGSH	EAN.MLSVLE IFAVSQGI.V
FGF1	KLL.....YC SNG.GHFLRI	LPDGTVDGTR	DRSDQHIQLQ LSAESVGE.V
FGF2	KRL.....YC KNG.GFFLRI	HPDGRVDGVR	EKSDPHIKLQ LQAEERGV.V
FGF9	RQL.....YC R.T.GFHLEI	FPNGTIQGTR	KDHSRFGILE FISIAVGL.V
FGF7	VRR.....LF CRT.QWYLRI	DKRGKVKGTQ	EMKNNYNIME IRTVAVGI.V
KGF2	WRK.....LF SFT.KYFLKI	EKNGKVSQTK	KENCPYSILE ITSVEIGV.V
FGF3	RRK.....LY CAT.KYHLQL	HPSGRVNGSL	.ENSAYSILE ITAVEVGI.V
FGF8	RRLIRTYQLY	SRTSGKHVQV	LANKRINAMA EDGDPPAKLI VETDTFGSRV

	151		200
FGF4	SIFGVASRFF	VAMSSKGKLY	G.SPFFTDEC TFKEILLPNN YNAYESYKYP
FGF6	SLFGVRSALF	VAMNSKGRLY	A.TPSFQEEC KFRETLLPNN YNAYESDLYQ
FGF5	GIRGVFSNKF	LAMSKKGKLY	A.SAKFTDDC KFRERFQENS YNTYASAIHR
FGF1	YIKSTETGQY	LAMDTDGLLY	G.SQTPNEEC LFLERLEENH YNTYISKKH.
FGF2	SIKGVCANRY	LAMKEDGRLL	A.SKCVTDEC FFFERLESNN YNTYRSRKY.
FGF9	SIRGVDSGLY	LGMNEKGELY	G.SEKLTQEC VFREQFEENW YNTYSSNLYK
FGF7	AIKGVSESEFY	LAMNKEGKLY	A.KKECNEDC NFKELILENH YNTYAS....
KGF2	AVKAINSNEY	LAMNKKGKLY	G.SKEFNNDK KLKERIEENG YNTYAS....
FGF3	AIRGLFSGRY	LAMNKRGRLY	A.SEHYSAEC EFVERIHELG YNTYASRLYR
FGF8	RVRGAETGLY	ICMNNKGKLI	AKSNGKGKDC VFTEIVLENN YTALQNAKY.

MATCH WITH FIG. 2C

FIG. 2B

MATCH WITH FIG. 2B

	201		250
FGF4	.....	GM.....FI ALSKNGKTKK G..NRVSPTM KVTHFLPRL.	
FGF6	.....	GT.....YI ALSKYGRVKR G..SKVSPIM TVTHFLPRI.	
FGF5	.....	TEKTGREWYV ALNKRKGAKR GCSPRVKPQH ISTHFLPRFK	
FGF1	.....	...AEKNWFV GLKKNNGSCKR G..PRTHYGQ KAILFLPLPV	
FGF2	.....	...T..SWYV ALKRTGQYKL G..SKTGPGQ KAILFLPMSA	
FGF9	HV.....	..DTGRRYYV ALNKDGTPRE G..TRTKRHQ KFTHFLPRPV	
FGF7	.....	AKW THNGGEM.FV ALNQKGIPVR G..KKTKKEQ KTAHFLPMAI	
KGF2	.....	FNW QHNGRQM.YV ALNGKGAPRR G..QKTRRKN TSAHFLPMVV	
FGF3	TVSSTPGARR	QPSAERLWYV SVNGKGRPRR G..FKTRRTQ KSSLFLPRVL	
FGF8	.....	.....EGWYM AFTRKGRPRK G..SKTRQHQ REVHFMKRLP	

	251		300
FGF4	.....	.....	.....
FGF6	.....	.....	.....
FGF5	QSEQPELSFT	VTVPEKKNPP SPIKSKIPLS APRKNTNSVK YRLKFRFG..	
FGF1	SSD.....	.....	.....
FGF2	KS.....	.....	.....
FGF9	DPDKVPELYK	DILSQS.....	.....
FGF7	T.....	.....	.....
KGF2	HS.....	.....	.....
FGF3	DHRDHEMVRQ	LQSGLP RPPG KGVQPRRRRQ KQSPDNLEPS HVQASRLGSQ	
FGF8	RGHHTTEQSL	RFEFLNYPPF TRSLRGSQRT WAPEPR.....	.....

MATCH WITH FIG. 2D

FIG. 2C

MATCH WITH FIG. 2C

	301
FGF4	.....
FGF6	.....
FGF5	.....
FGF1	.....
FGF2	.....
FGF9	.....
FGF7	.....
KGF2	.....
FGF3	LEASAH
FGF8	.....

FIG.2D

GGAATTC	CCGG	GAAGAGAGGG	AAGAAAACAA	CGGCGACTGG	GCAGCTGCCT	CCACTTCTGA	60			
CAACTCCAAA	GGGATATACT	TGTAGAAGTG	GCTCGCAGGC	TGGGGCTCCG	CAGAGAGAGA	120				
CCAGAAGGTG	CCAACCGCAG	AGGGGTGCAG	ATATCTCCCC	CTATTCCCCA	CCCCACCTCC	180				
CTTGGGTTTT	GTTCAACCGTG	CTGTCATCTG	TTTTTCAGAC	CTTTTTGGCA	TCTAACATGG	240				
TGAAGAAAGG	AGTAAAGAAG	AGAACAAAGT	AACTCCTGGG	GGAGCGAAGA	GCGCTGGTGA	300				
CCAACACCAC	CAACGCCACC	ACCAGCTCCT	GCTGCTGCGG	CCACCCACGT	CCACCATTTA	360				
CCGGGAGGCT	CCAGAGGCGT	AGGCAGCGGA	TCCGAGAAAG	GAGCGAGGGG	AGTCAGCCGG	420				
CTTTTCCGAG	GAGTTATGGA	TGTTGGTGCA	TTCACTTCTG	GCCAGATCCG	CGCCCAGAGG	480				
GAGCTAACCA	GCAGCCACCA	CCTCGAGCTC	TCTCCTTGCC	TTGCATCGGG	TCTTACCCTT	540				
CCAGTATGTT	CCTTCTGATG	AGACAATTTT	CAGTGCCGAG	AGTTTCAGTA	CA ATG	595				
					Met					
TGG AAA	TGG ATA	CTG ACA	CAT CAT	TGT GCC	TCA GCC	TTT CCC	CAC CTG	CCC	643	
Trp Lys	Trp Ile	Leu Thr	His His	Cys Cys	Ala Ser	Ala Phe	Pro His	Leu Pro		
GGC TGC	TGC TGC	TGC TGC	TGC TGC	TTT TTT	TTG TTG	CTG TTC	TTG GTG	TCT TCC	GTC	691
Gly Cys	Cys Cys	Cys Cys	Cys Cys	Phe Phe	Leu Leu	Leu Phe	Leu Val	Ser Ser	Val	
CCT GTC	ACC TGC	CAA GCC	CTT CTT	GGT CAG	GAC ATG	GTG TCA	CCA GAG	GCC	739	
Pro Val	Thr Cys	Gln Ala	Leu Leu	Gly Gln	Asp Met	Val Ser	Pro Glu	Ala		
ACC AAC	TCT TCT	TCC TCC	TCC TCC	TTC TCC	TCT CCT	TCC AGC	GCG GGA	AGG	787	
Thr Asn	Ser Ser	Ser Ser	Ser Ser	Phe Ser	Ser Pro	Ser Ser	Ala Gly	Arg		
CAT GTG	CGG AGC	TAC TAC	AAT CAC	CTT CAA	GGA GAT	GTC CGC	TGG AGA	AAG	835	
His Val	Arg Ser	Tyr Tyr	Asn His	Leu Leu	Gln Gly	Asp Val	Arg Trp	Arg Lys		
CTA TTC	TCT TTC	ACC AAG	TAC TTT	CTC CTC	AAG ATT	GAG AAG	AAC GGG	AAG	883	
Leu Phe	Ser Phe	Thr Lys	Tyr Phe	Leu Leu	Lys Ile	Glu Lys	Asn Gly	Lys		
GTC AGC	GGG ACC	AAG AAG	GAG AAC	TGC CCG	TAC AGC	ATC CTG	GAG ATA	931		
Val Ser	Gly Thr	Lys Lys	Glu Asn	Cys Pro	Tyr Ser	Ile Leu	Glu Ile			
ACA TCA	GTA GAA	ATC GGA	GTT GTT	GCC GTC	AAA GCC	ATT AAC	AGC AAC	979		
Thr Ser	Val Glu	Ile Ile	Gly Val	Val Ala	Val Lys	Ala Ile	Asn Ser	Asn		
TAT TAC	TTA GCC	ATG AAC	AAG AAG	GGG AAA	CTC TAT	GGC TCA	AAA GAA	1027		
Tyr Tyr	Leu Ala	Met Asn	Lys Lys	Gly Lys	Leu Tyr	Gly Ser	Lys Glu			
TTT AAC	AAT GAC	TGT AAG	CTG AAG	GAG AGG	ATA GAG	GAA AAT	GGA TAC	1075		
Phe Asn	Asn Asp	Cys Cys	Lys Leu	Lys Glu	Arg Ile	Glu Glu	Asn Gly	Tyr		

FIG. 3A



AAT ACC TAT GCA TCA TTT AAC TGG CAG CAT AAT GGG AGG CAA ATG TAT Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr	1123
GTG GCA TTG AAT GGA AAA GGA GCT CCA AGG AGA GGA CAG AAA ACA CGA Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg	1171
AGG AAA AAC ACC TCT GCT CAC TTT CTT CCA ATG GTG GTA CAC TCA Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser	1216
TAGAGGAAGG CAACGTTTGT GGATGCAGTA AAACCAATGG CTCTTTTGCC AAGAATAGTG	1276
GATATTCTTC ATGAAGACAG TAGATTGAAA GGCAAAGACA CGTTGCAGAT GTCTGCTTGC	1336
TTAAAAGAAA GCCAGCCTTT GAAGGTTTTT GTATTCACTG CTGACATATG ATGTTCTTTT	1396
AATTAGTTCT GTGTCATGTC TTATAATCAA GATATAGGCA GATCGAATGG GATAGAAGTT	1456
ATTCCCAAGT GAAAAACATT GTGGCTGGGT TTTTGTGTGT TGTGTCAAG TTTTGTGTTT	1516
TAAACCTCTG AGATAGAACT TAAAGGACAT AGAACAATCT GTTGAAAGAA CGATCTTCGG	1576
GAAAGTTATT TATGGAATAC GAACTCATAT CAAAGACTTC ATTGCTCATT CAAGCCTAAT	1636
GAATCAATGA ACAGTAATAC GTGCAAGCAT TTAAGTGGAA GCACTTGGGT CATATCATAT	1696
GCACAACCAA AGGAGTTCTG GATGTGGTCT CATGGAATAA TTGAATAGAA TTTAAAAATA	1756
TAAACATGTT AGTGTGAAAC TGTTCTAACA ATACAAATAG TATGGTATGC TTGTGCATTC	1816
TGCCTTCATC CCTTTCTATT TCTTTCTAAG TTATTTATTT AATAGGATGT TAAATATCTT	1876
TTGGGGTTTT AAAGAGTATC TCAGCAGCTG TCTTCTGATT TATCTTTTCT TTTTATTCAG	1936
CACACCACAT GCATGTTTAC GACAAAGTGT TTTTAAACT TGGCGAACAC TTCAAAAATA	1996
GGAGTTGGGA TTAGGGAAGC AGTATGAGTG CCCGTGTGCT ATCAGTTGAC TTAATTTGCA	2056
CTTCTGCAGT AATAACCATC AACAATAAAT ATGGCAATGC TGTGCCATGG CTTGAGTGAG	2116
AGATGTCTGC TATCATTTGA AACATATAT TACTCTCGAG GCTTCCTGTC TCAAGAAATA	2176
GACCAGAAGG CCAAATTCTT CTCTTTCAAT ACATCAGTTT GCCTCCAAGA ATATACTAAA	2236
AAAAGGAAAA TTAATTGCTA AATACATTTA AATAGCCTAG CCTCATTATT TACTCATGAT	2296
TTCTTGCCAA ATGTCATGGC GGTAAAGAGG CTGTCCACAT CTCTAAAAAC CCTCTGTAAA	2356
TTCCACATAA TGCATCTTTC CCAAAGGAAC TATAAAGAAT TTGGTATGAA GCGCAACTCT	2416

FIG.3B

CCCAGGGGCT TAACTGAGC AAATCAAATA TATACTGGTA TATGTGTAAC CATATACAAA	2476
AACCTGTTCT AGCTGTATGA TCTAGTCTTT ACAAACCAA ATAAACTTG TTTTCTGTAA	2536
ATTTAAAGAG CTTTACAAGG TTCCATAATG TAACCATATC AAAATTCATT TTGTTAGAGC	2596
ACGTATAGAA AAGAGTACAT AAGAGTTTAC CAATCATCAT CACATTGTAT TCCACTAAAT	2656
AAATACATAA GCCTTATTTG CAGTGTCTGT AGTGATTTTA AAAATGTAGA AAAATACTAT	2716
TTGTTCTAAA TACTTTTAAG CAATAACTAT AATAGTATAT TGATGCTGCA GTTTTATCTT	2776
CATATTTCTT GTTTTGAAAA AGCATTTTAT TGTTTGACA CAGTATTTTG GTACAAAAAA	2836
AAAGACTCAC TAAATGTGTC TTAATAAGT TTAACCTTG GAAATGCTGG CGTTCTGTGA	2896
TTCTCCAACA AACTTATTTG TGCAATACT TAACCAGCAC TTCCAGTTAA TCTGTTATTT	2956
TTAAAAATTG CTTTATTAAG AAATTTTTTG TATAATCCCA TAAAAGGTCA TATTTTCCC	3016
ATTCTTCAA AAAACTGTAT TTCAGAAGAA ACACATTGA GGCAGTGTCT TTTGGCTTAT	3076
AGTTTAAATT GCATTTATC ATACTTTGCT TCCAATTGC TTTTGGCAA ATGAGATTAT	3136
AAAAATGTTT AATTTTTGTG GTTGGAACTT GGATGTTAAA ATTTAATTGG TAACTCAGTC	3196
TGTGAGCTAT AATGTAATGC ATTCCTATCC AAATAAGTA TCTTTTTTTC CTTTATGTTG	3256
AAATAATAAT GGCACCTGAC ACATAGACAT AGACCACCCA CAACCTAAAT TAAATGTTTG	3316
GTAAGACAAA TACACATTGG ATGACCACAG TAACAGCAAA CAGGGCACAA ACTGGATTCT	3376
TATTTACAT AGACATTTAG ATTACTAAAG AGGGCTATGT GTAAACAGTC ATCATTATAG	3436
TACTCAAGAC ACTAAACAG CTTCTAGCCA AATATATTAA AGCTTGCAGA GGCCAAAAAT	3496
AGAAAACATC TCCCCTGTCT CTCCCACATT TCCCTCACAG AAAGACAAAA AACCTGCCTG	3556
GTGCAGTAGC TCACACCTGT AATCCCAGCA GTTTGGGAGA CTGTGGGAAG ATGGCTTGAG	3616
TCCAGGAGTT CTAGACAGGC CTGAGAAACC TAGTGAGACA TCCTTCTCTT AAACAAAACA	3676
AAACAAAACA AATGTAGCCA TGCCTGGTGG CATATACCTG TGGTCCCAAC TACTCAGGAG	3736
GCTGAAACGG AAGGATCTCT TGGGCCCCAG GAGTTTGAGG CTGCAGTGAG CTATAATCTT	3796
GCCATTGCAC TCCAGCCTGG GTGAAAAAGA GCCAGAAAGA AAGGAAAGAG AGAAAAGAGA	3856
AAAGAAAGAG AGAAAAGACA GAAAGACAGG AAGGAAGGAA GGAAGGAAGG AAGGAAGGAA	3916
GGAAGCAAGG AAAGAAGGAA GGAAGGAAAG AAGGGAGGGA AGGAAGGAGA GAGAAAGAAA	3976
GATTGTTTGG TAAGGAGTAA TGACATTCTC TTGCATTTAA AAGTGGCATA TTTGCTTGAA	4036

FIG.3C

ATGGAAATAG AATTCTGGTC CCTTTTGCAA CTACTGAGA AAAAAAAG CAGTTCAGC	4096
CCTGAATGTT GTAGATTGA AAAAAAAAAA AAAAAAATC GAGGGGGGGC CCGTACCCAA	4156
TTCGCCCTAT AGTGAGTCGT A	4177

FIG.3D

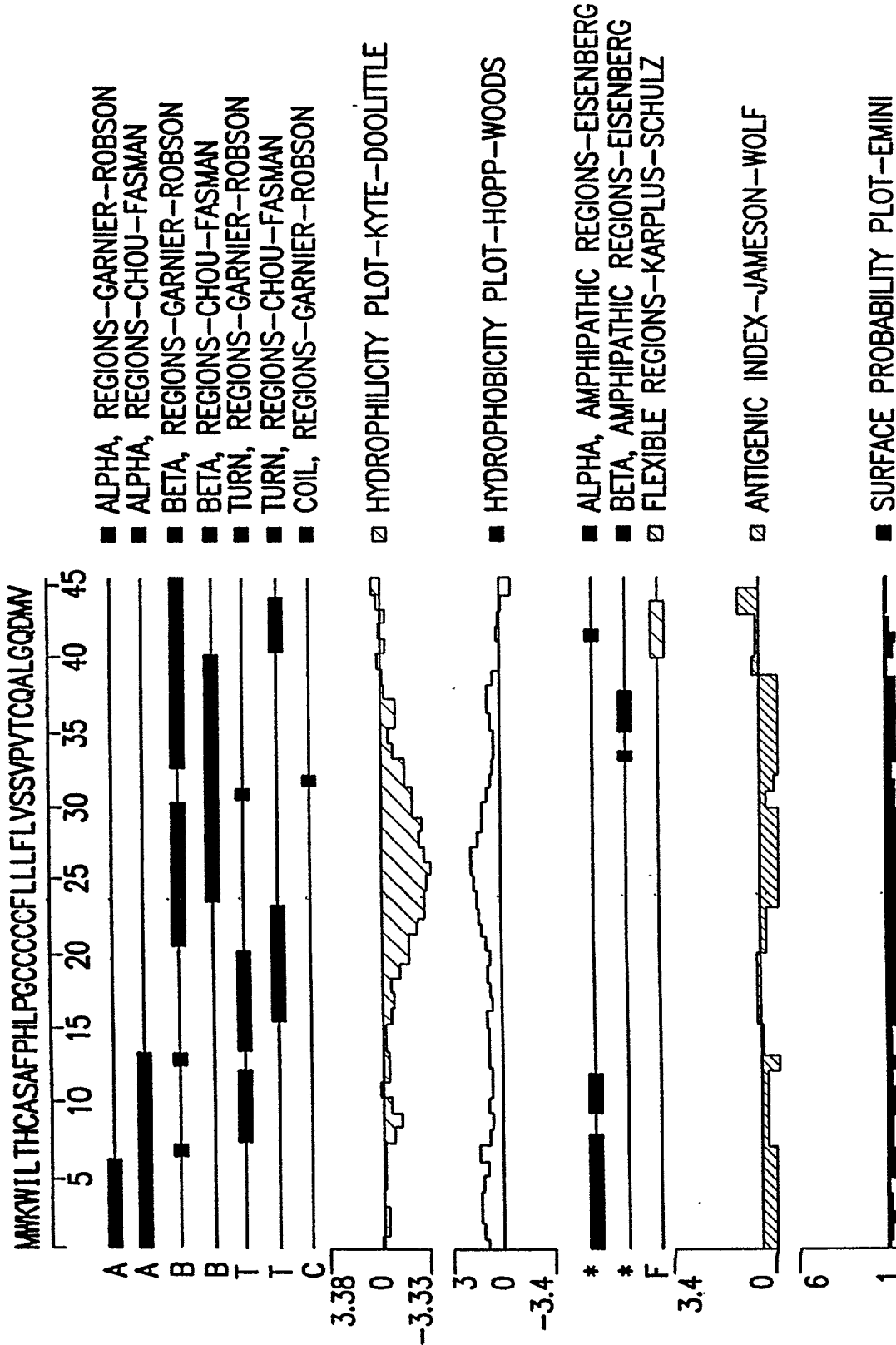


FIG.4A

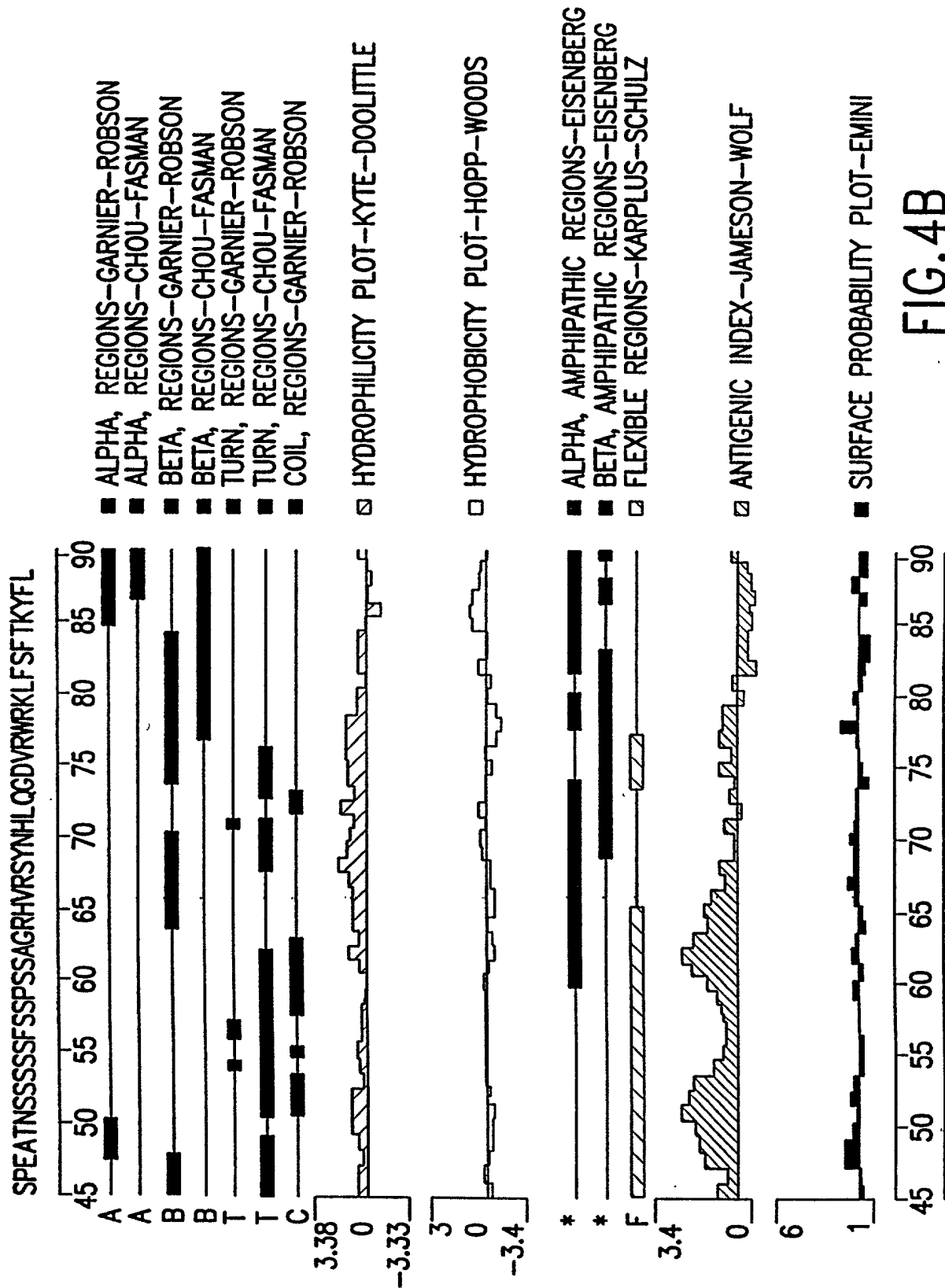
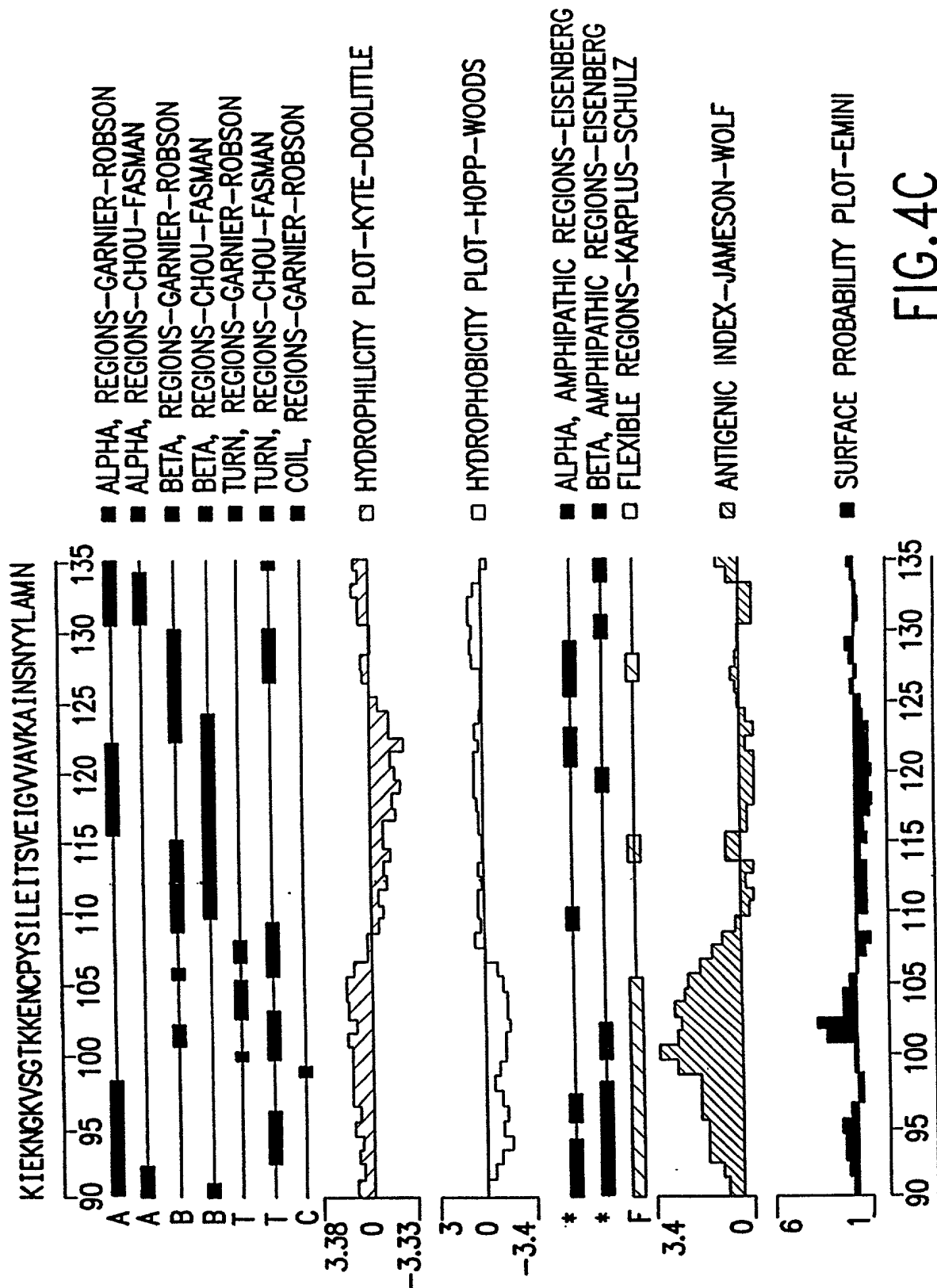


FIG.4B



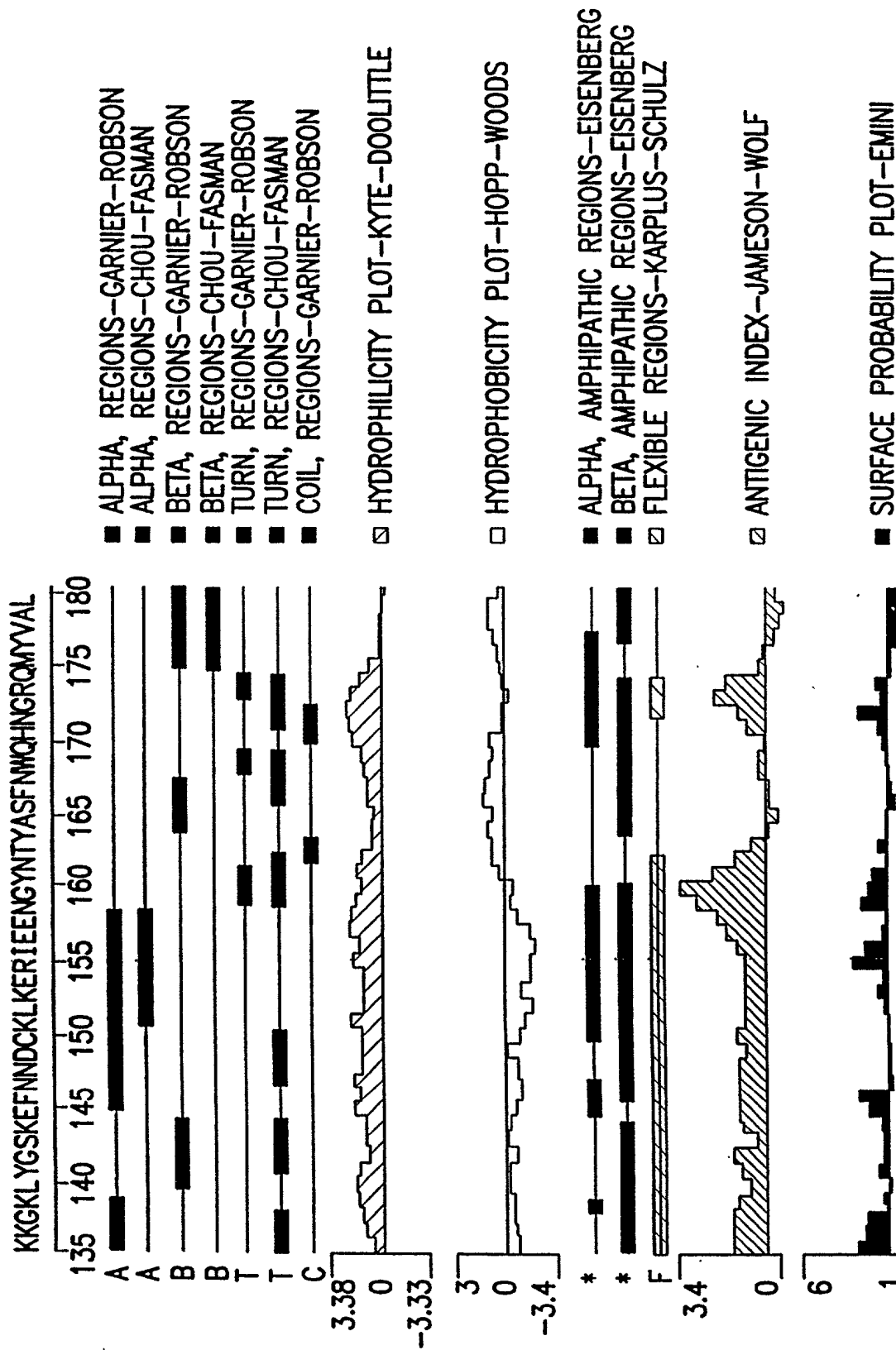
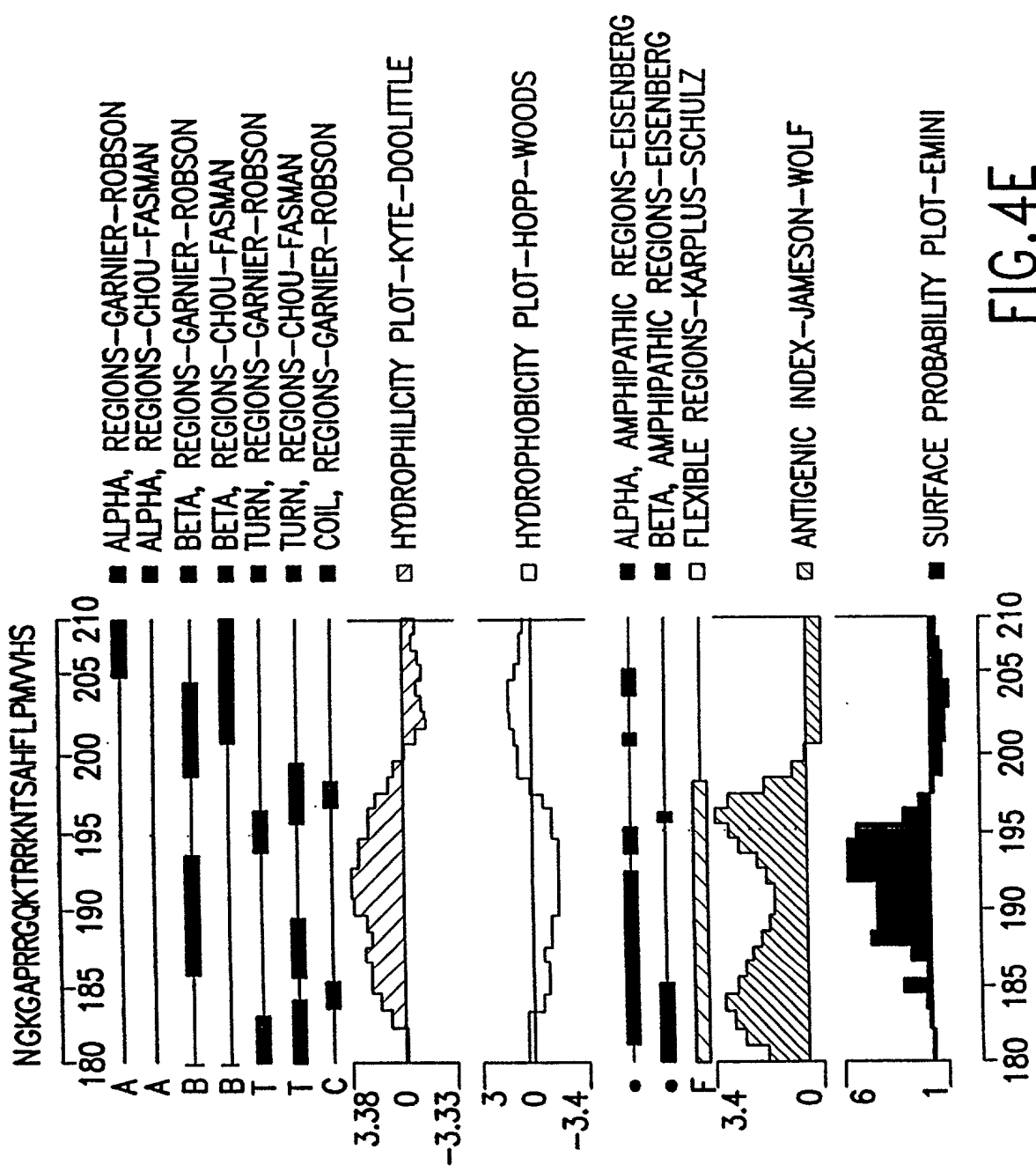


FIG.4D





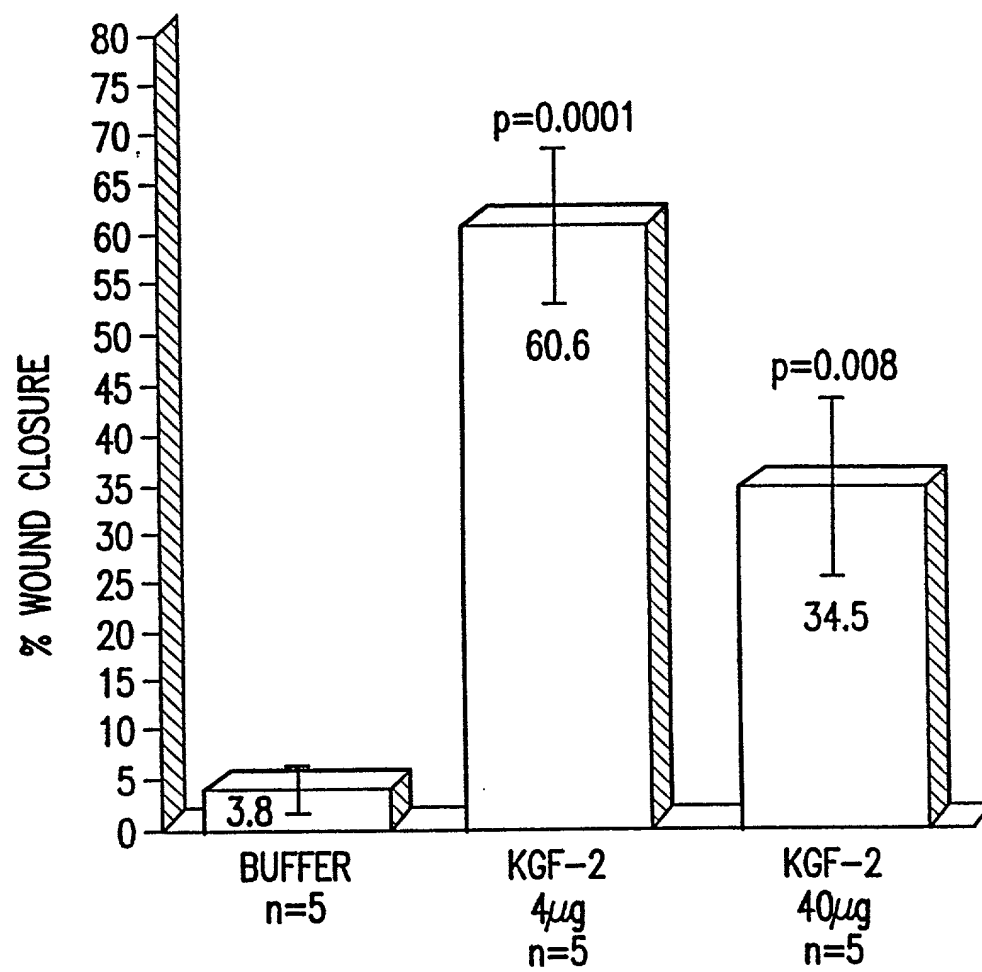


FIG.5

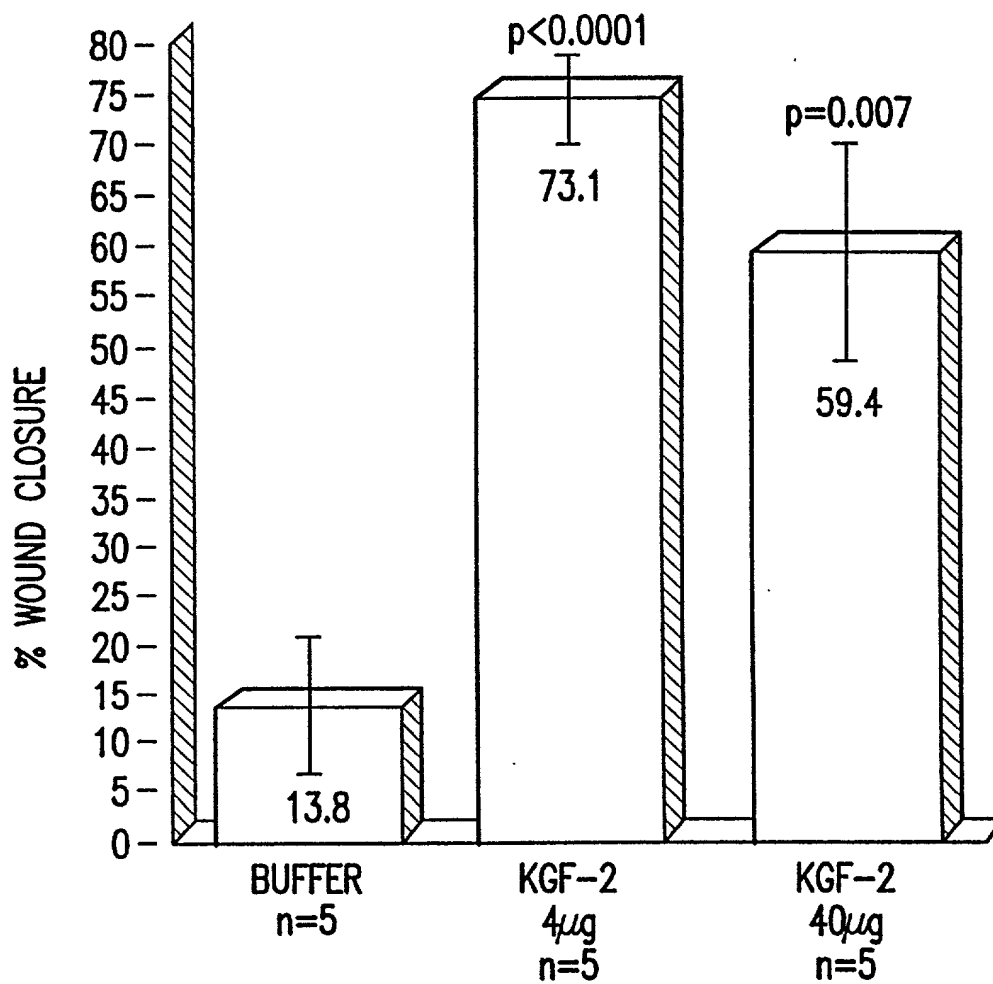


FIG.6

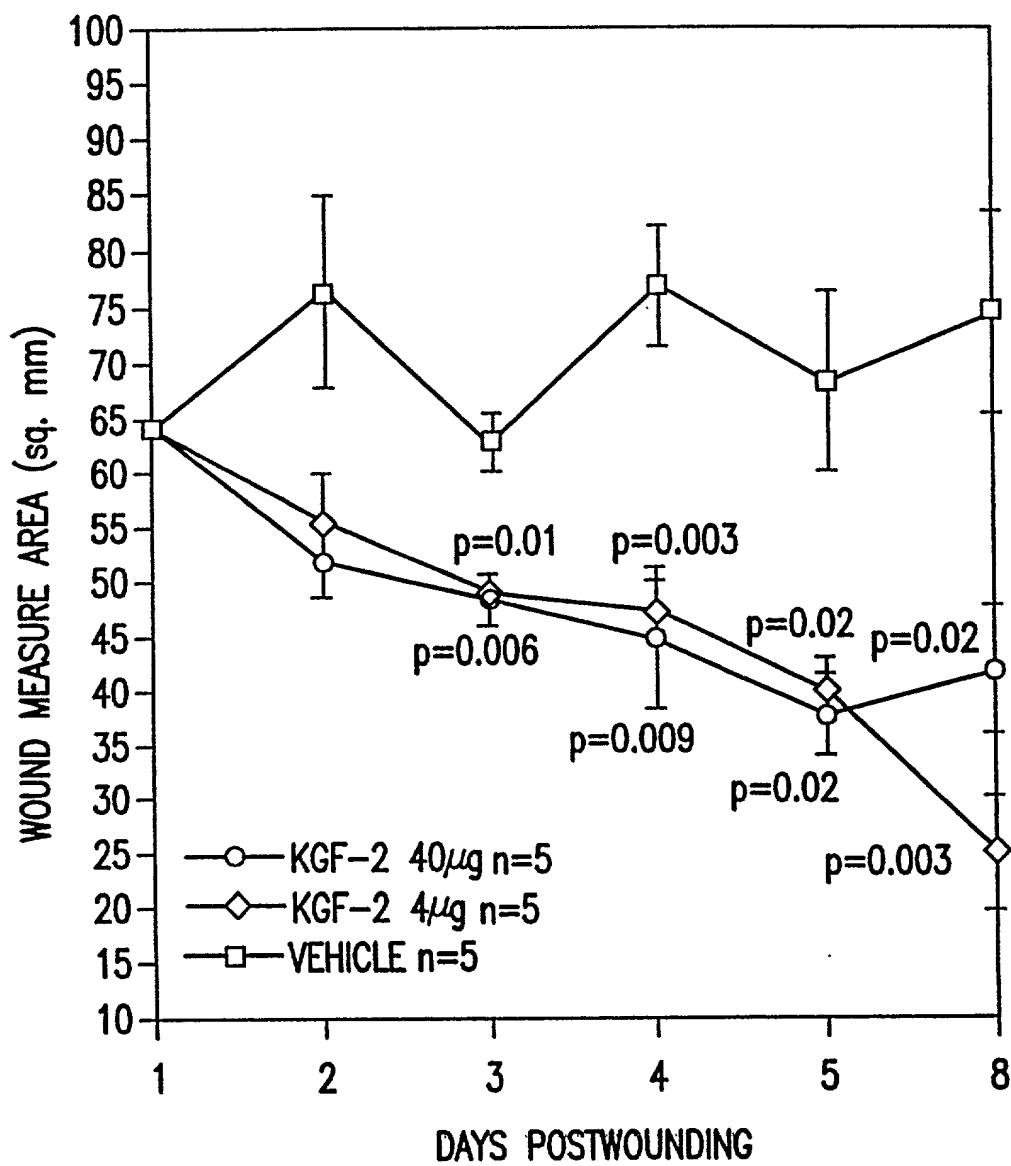


FIG.7

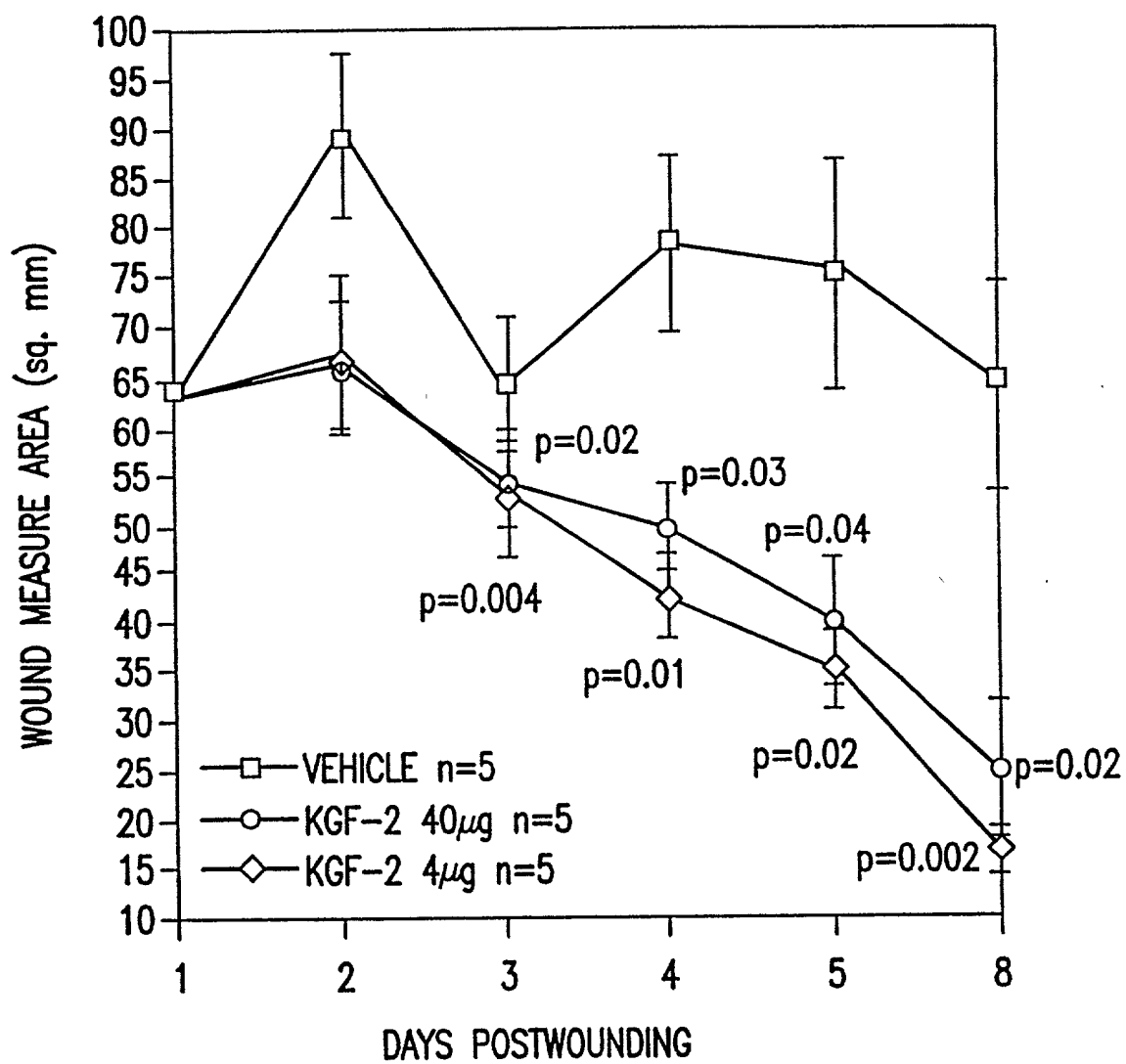
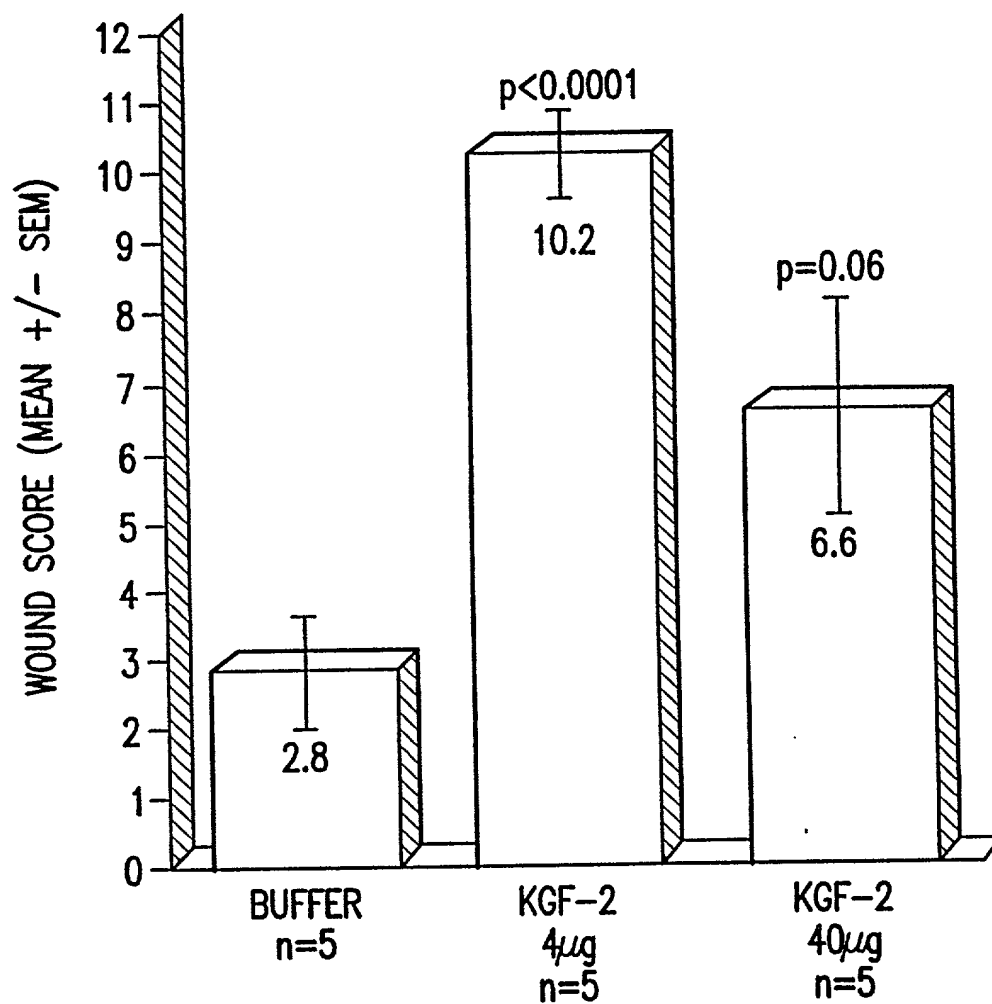
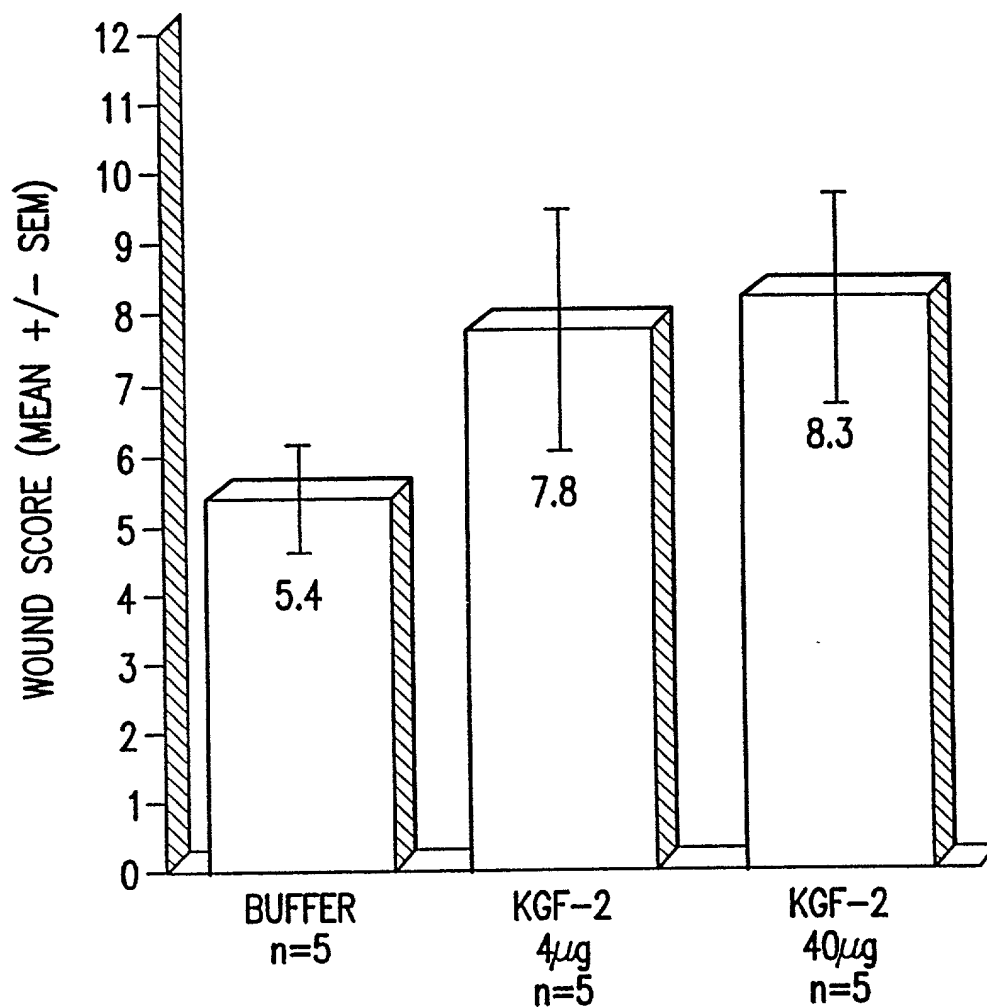


FIG.8



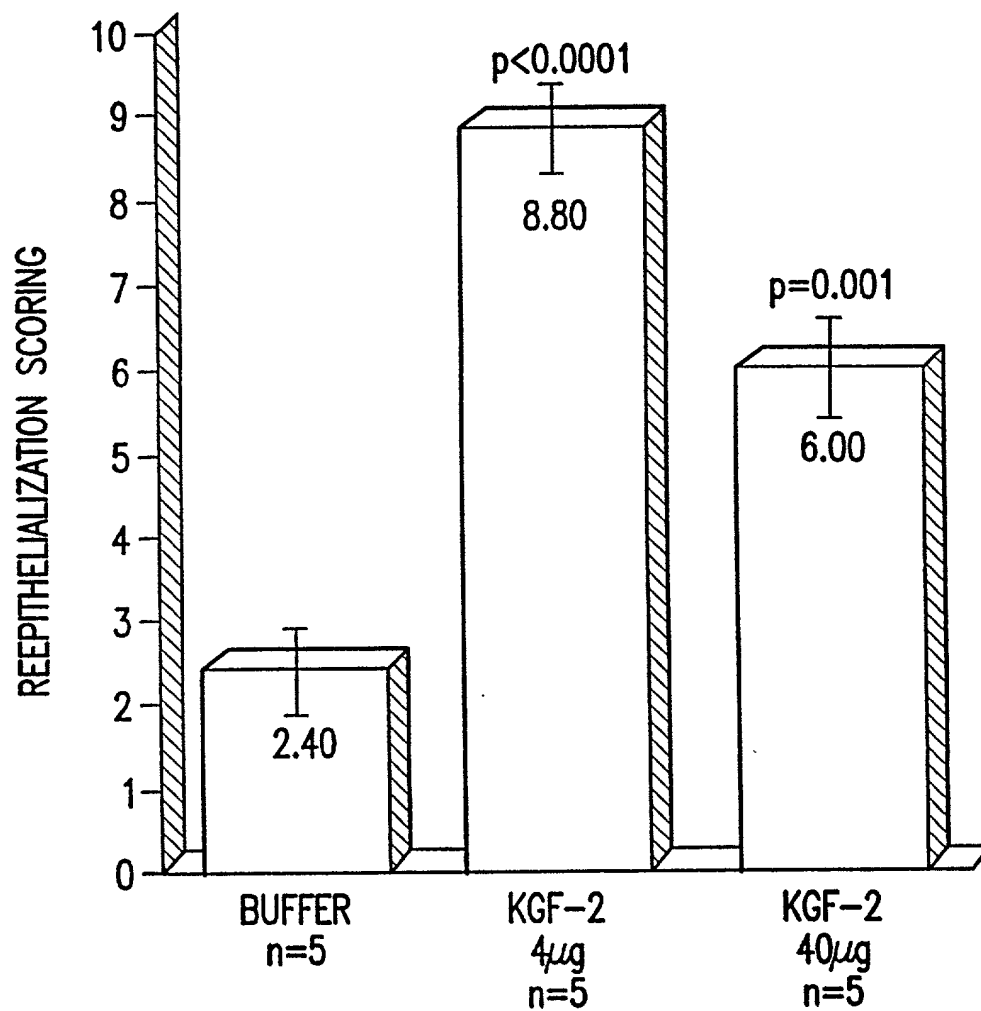
1-3 MINIMAL CELL ACCUMULATION, NO GRANULATION  
 4-6 IMMATURE GRANULATION, INFLAMMATORY CELLS, CAPILLARIES  
 10-12 FIBROBLASTS, COLLAGEN, EPITHELIUM

FIG.9



1-3 MINIMAL CELL ACCUMULATION, NO GRANULATION  
 4-6 IMMATURE GRANULATION, INFLAMMATORY CELLS, CAPILLARIES  
 7-9 GRANULATION TISSUE, CELLS, FIBROBLASTS, NEW EPITHELIUM  
 10-12 FIBROBLASTS, COLLAGEN, EPITHELIUM

FIG.10



ANTI-CYTOKERATIN IMMUNOSTAINING  
0-NO CLOSURE  
5-SLIGHT TO MODERATE CLOSURE  
10-COMPLETE CLOSURE

FIG.11

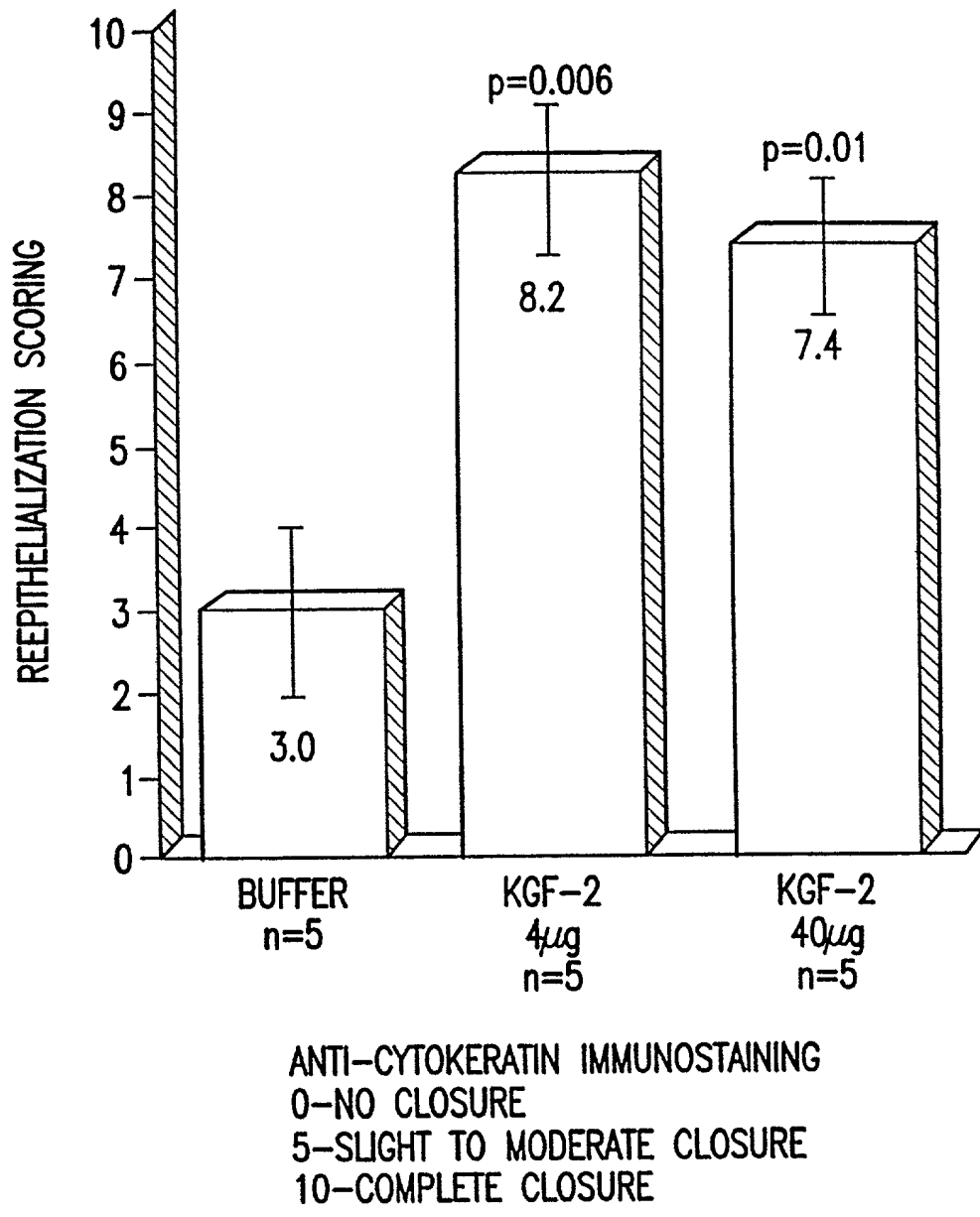
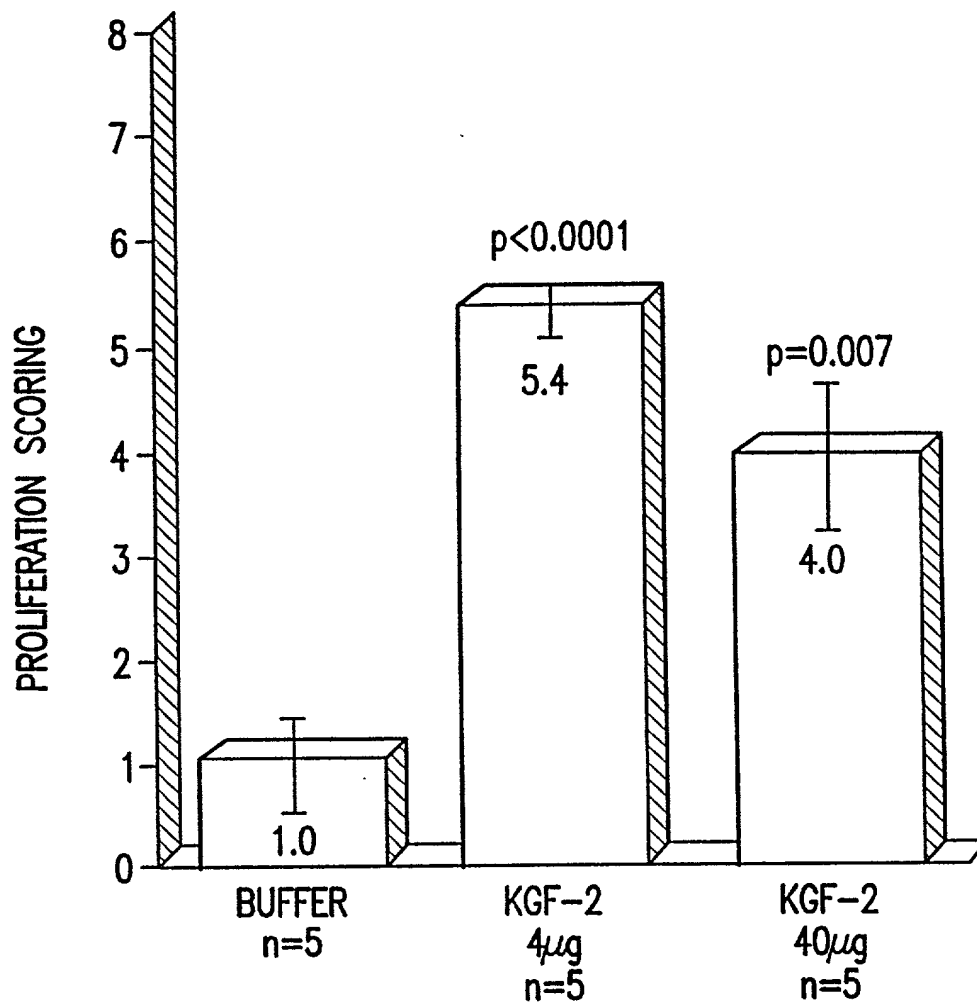


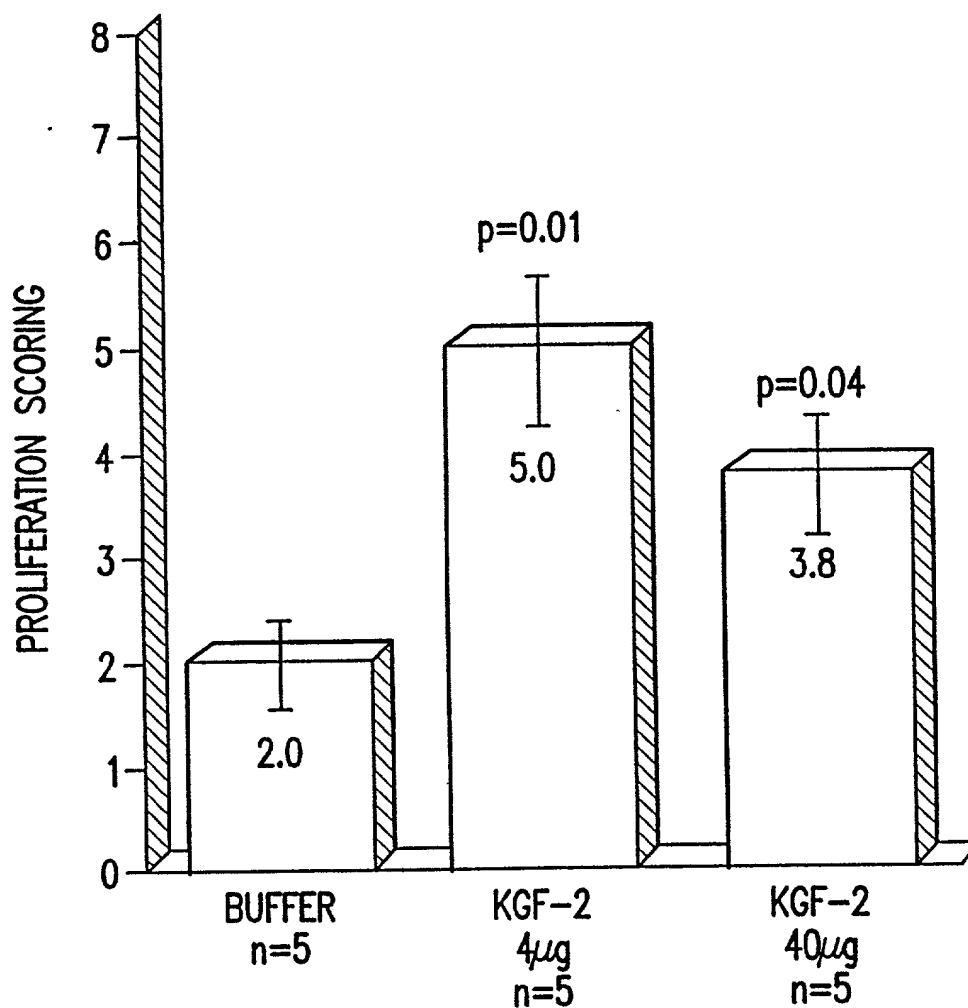
FIG.12





PCNA SCORING  
0-2 SLIGHT PROLIFERATION  
3-5 MODERATE PROLIFERATION  
6-8 INTENSE PROLIFERATION

FIG.13



PCNA SCORING  
 0-2 SLIGHT PROLIFERATION  
 3-5 MODERATE PROLIFERATION  
 6-8 INTENSE PROLIFERATION

FIG.14

ATGAGAGGATCGCATCACCATCACCATCACGGATCCTGCCAGGCTCTGGGTC  
 AGGACATGGTTTCTCCGGAAGCTACCAACTCTTCCTCTTCCTCTTTCTCTTCCC  
 CGTCTTCOGCTGGTCGTACGTTTCGTTCTTACAACCACCTGCAGGGTGACGTTT  
 GTTGGCGTAAACTGTTCTCTTTACCAAATACTTCCTGAAAATCGAAAAA  
 AACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCCGTACAGCATCCTG  
 GAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAG  
 CAACTATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAG  
 AATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGAT  
 ACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTAT  
 GTGGCATTGAaTGGAAAAGGAGCTCCAaGGAGAGGACAGAAAACACGAAG  
 GAAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MRGSHHHHHHGSCQALGQDMVSPEATNSSSSSFSSPSSAGRHVRSYNHLQGD  
 VRWRKLFSTKYFLKIEKNGKVSGETTKENCYPYSILEITSVEIGVVAVKAINSN  
 YYLAMNKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVA  
 LNGKGAPRRGQKTRRKNTSAHFLPMVVHS

kgf-2 synthetic cys37 Bam HI  
AAAGGATCCTGCCAGGCTCTGGGTCAGGACATG

FIG.15

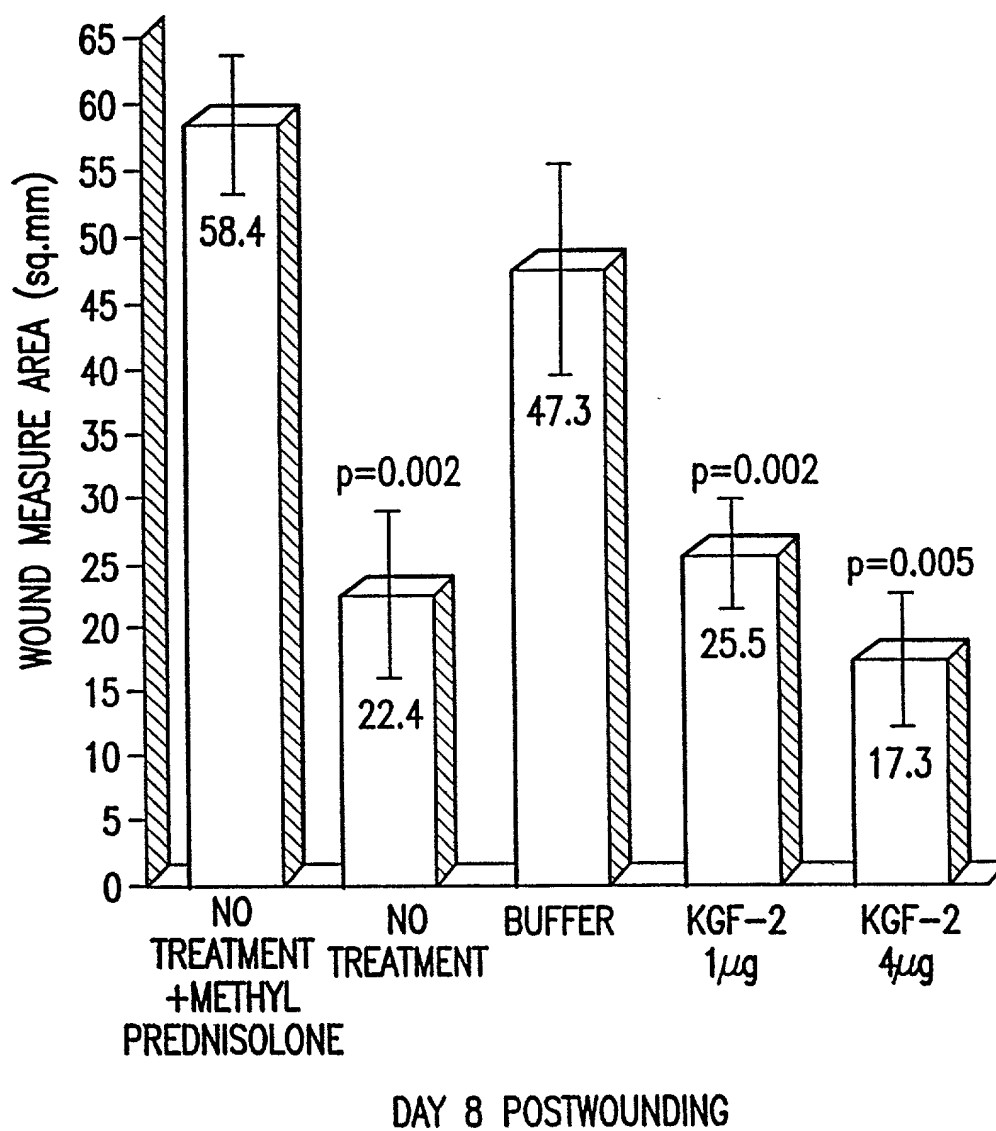
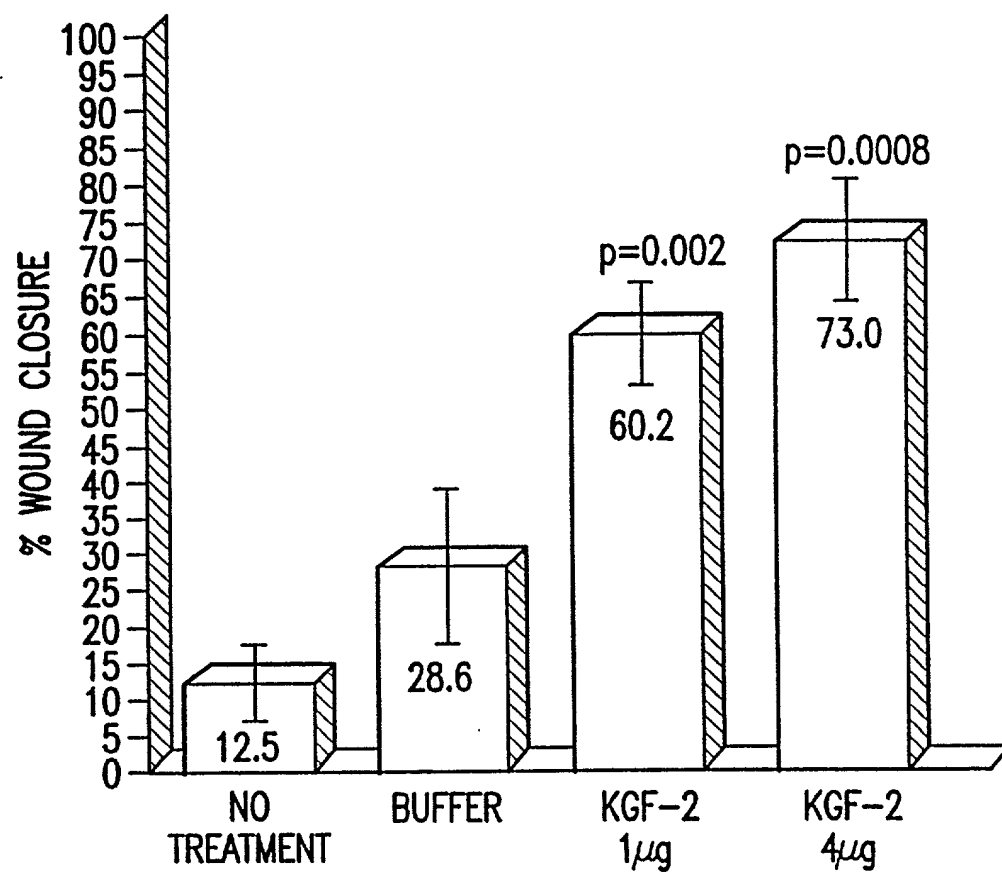


FIG.16



GLUCOCORTICOID TREATED ANIMALS

FIG.17

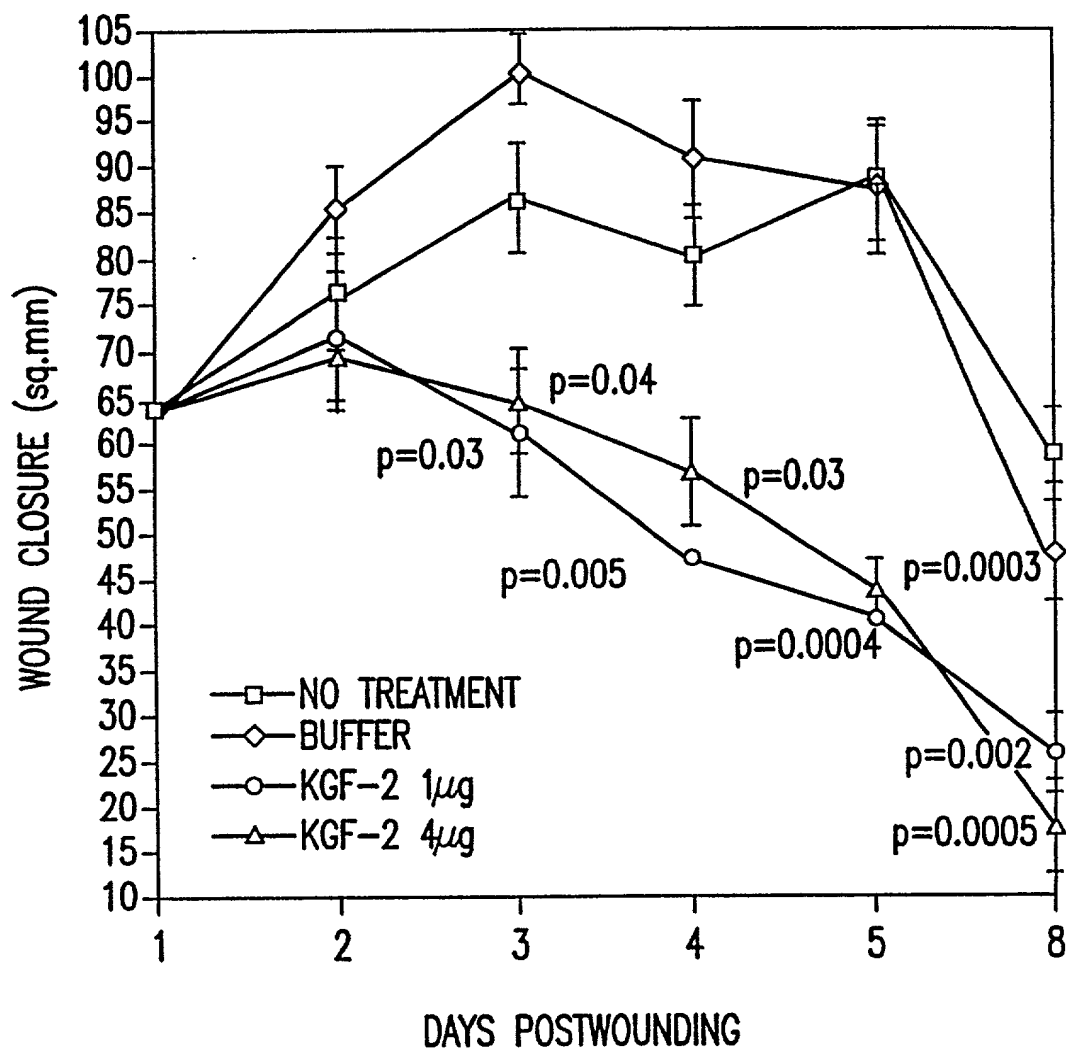


FIG.18

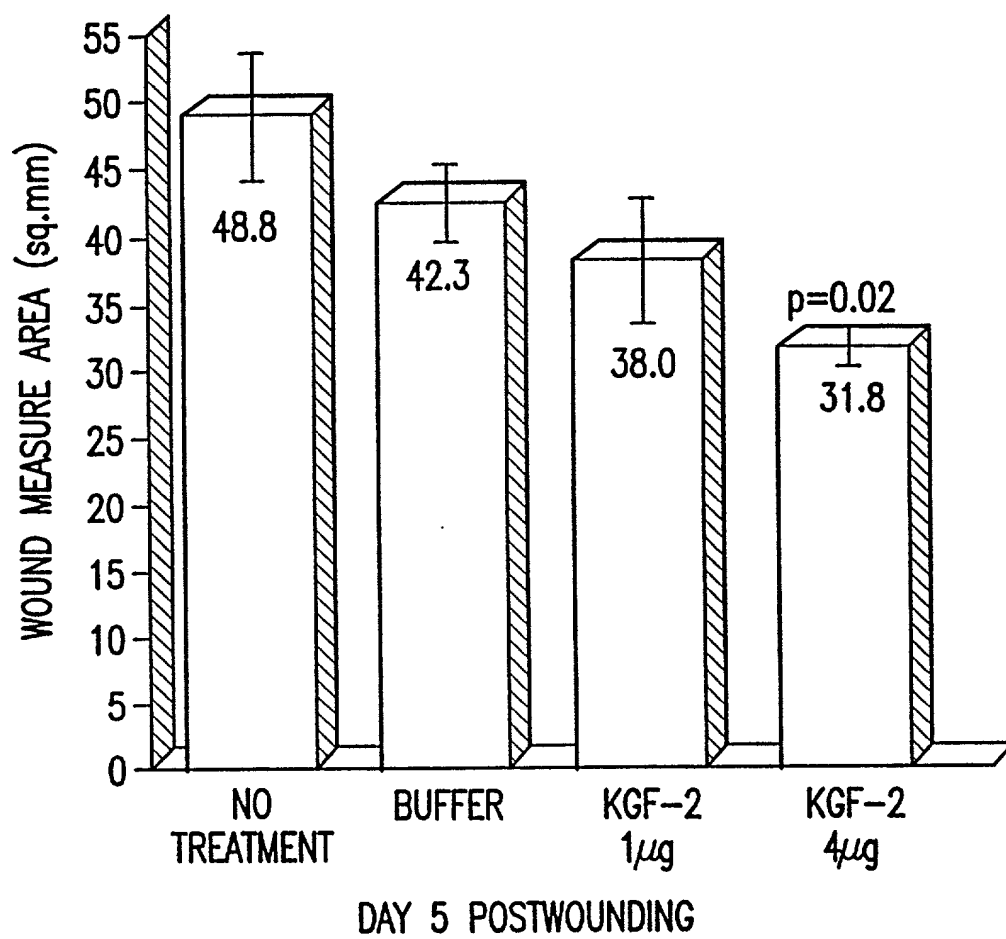
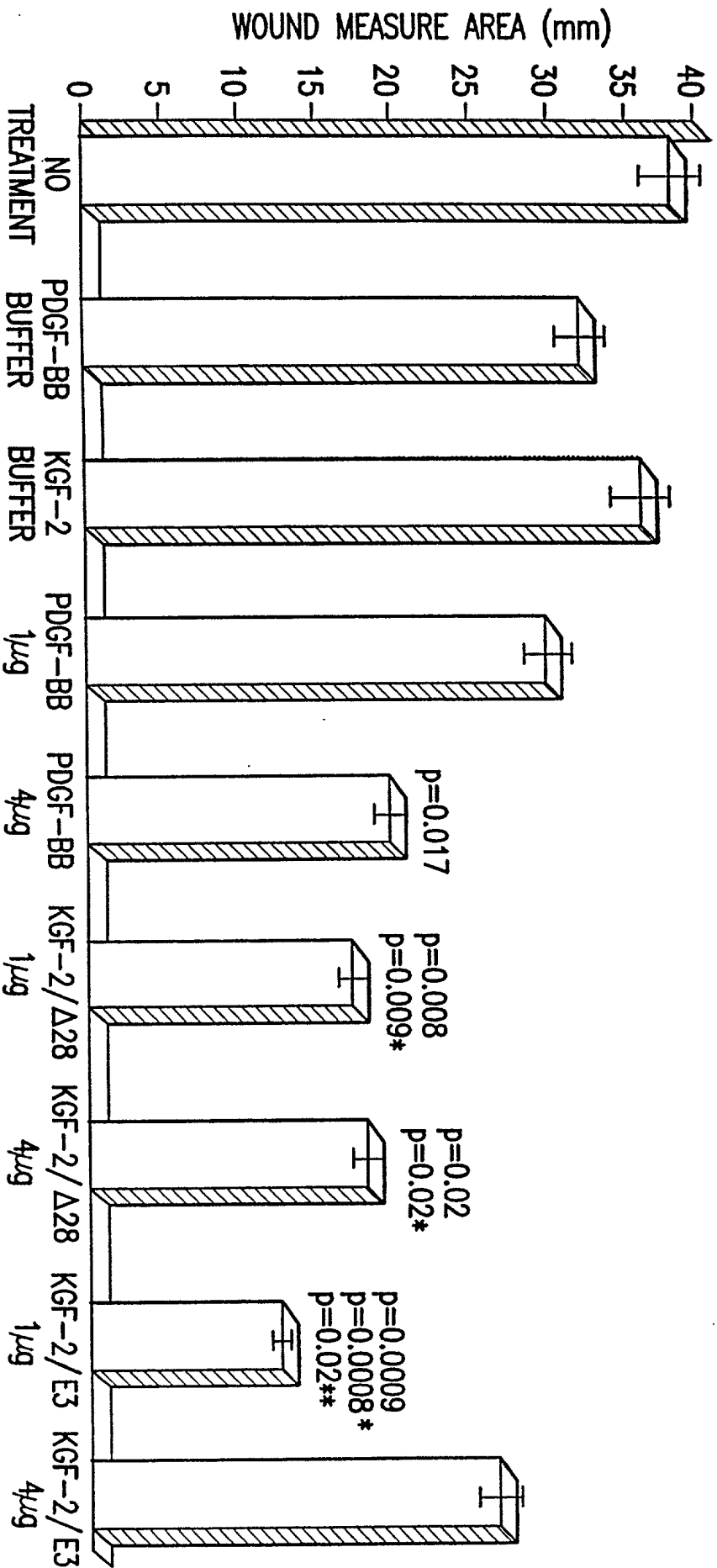


FIG.19A



DAY 10 POSTWOUNDING

FIG.19B



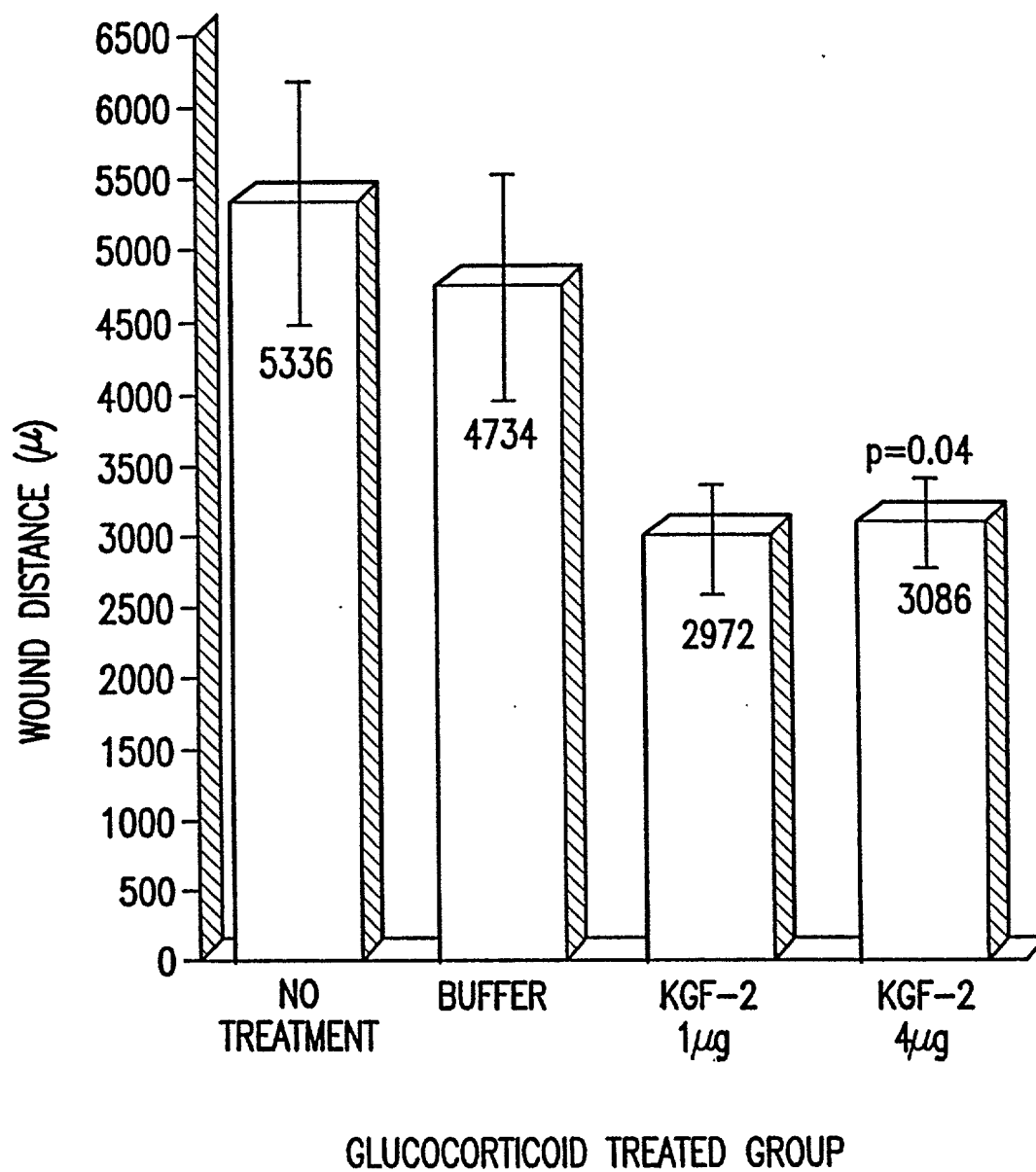


FIG.20

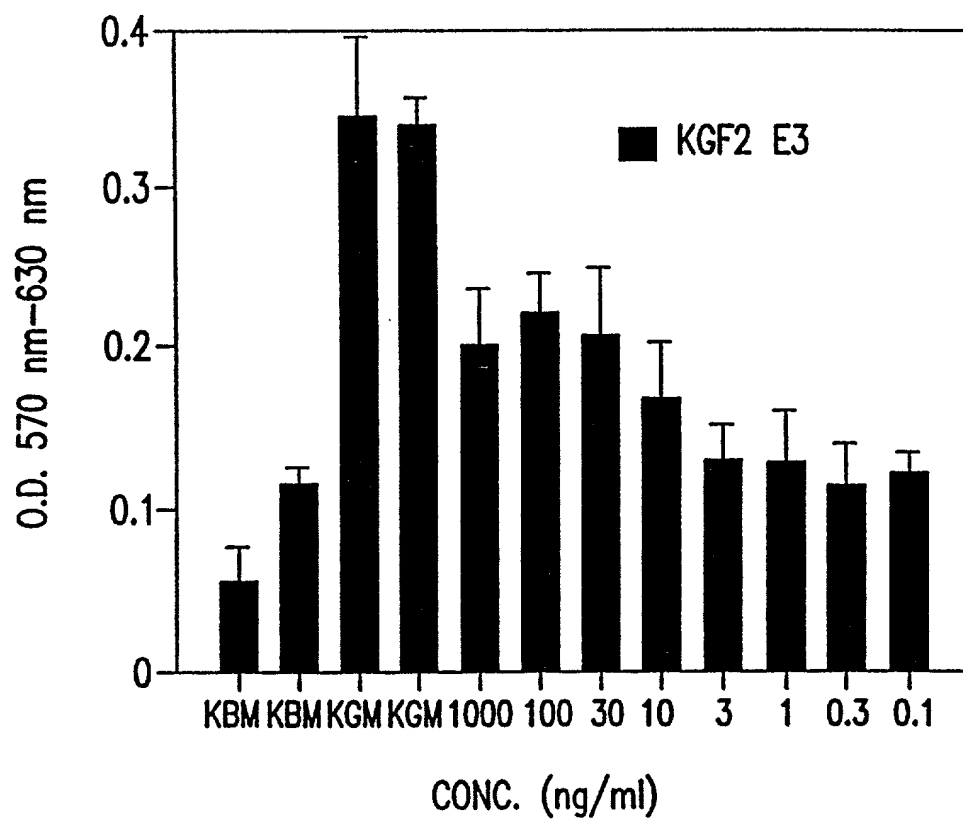


FIG.21A

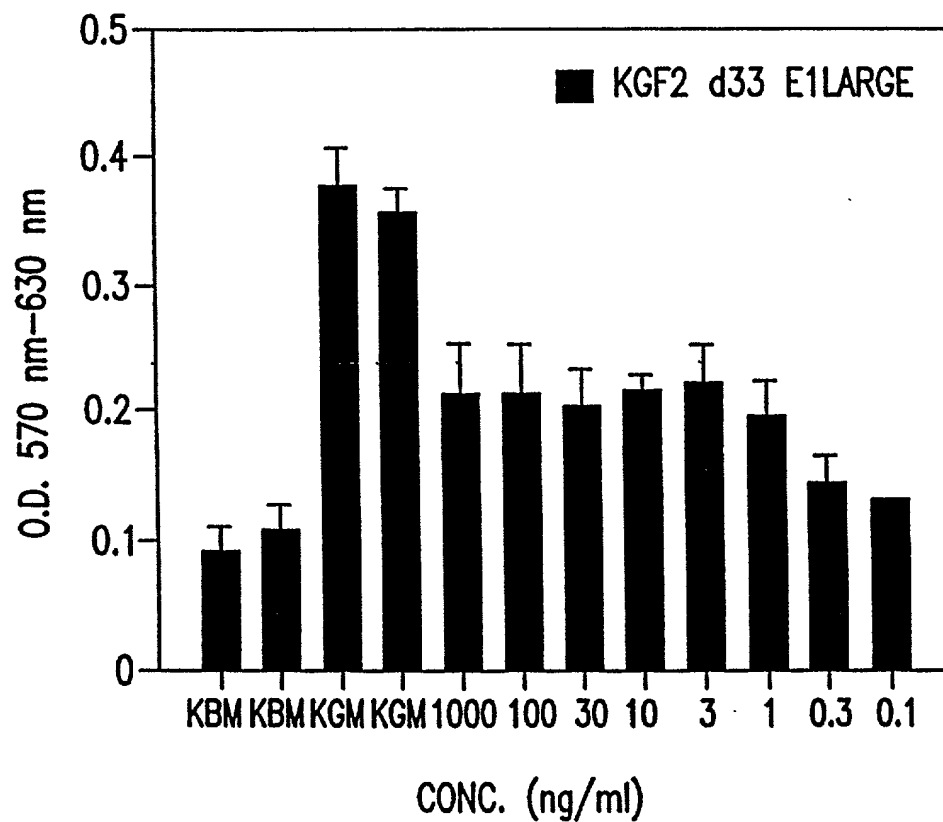


FIG.21B

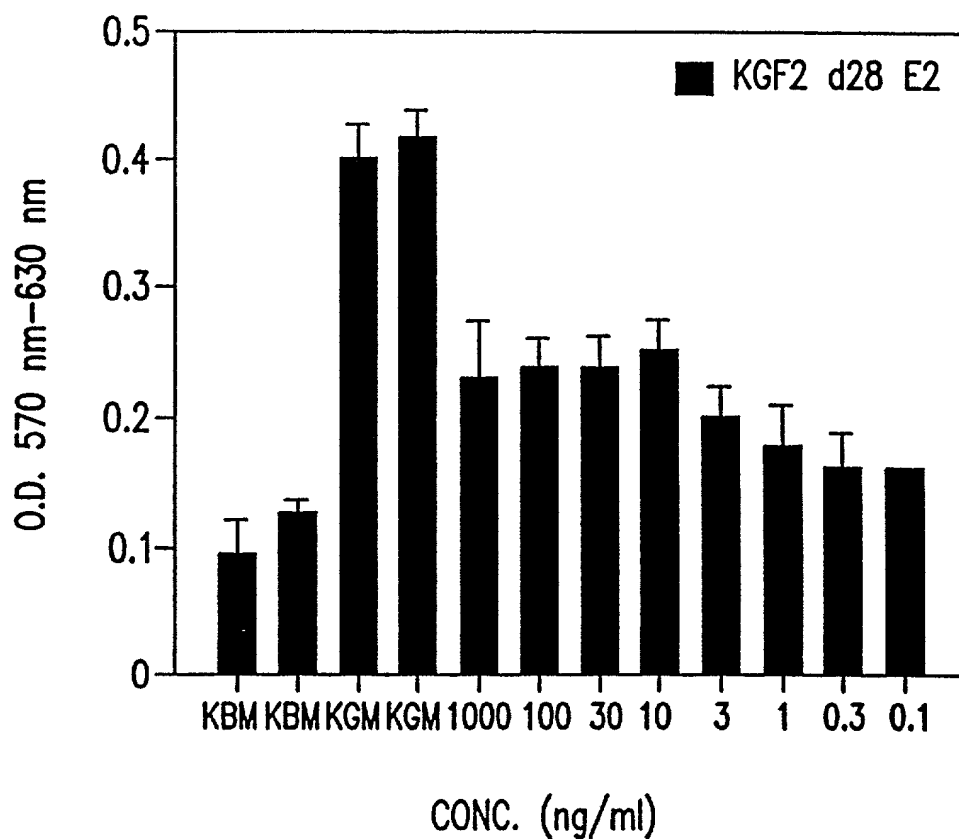


FIG.21C

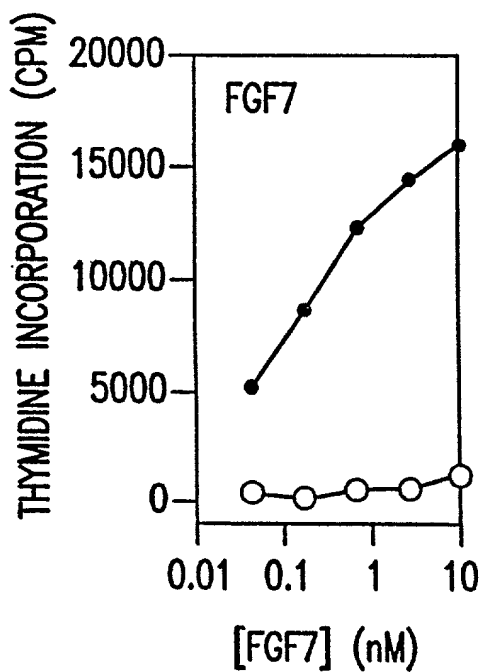


FIG.22A

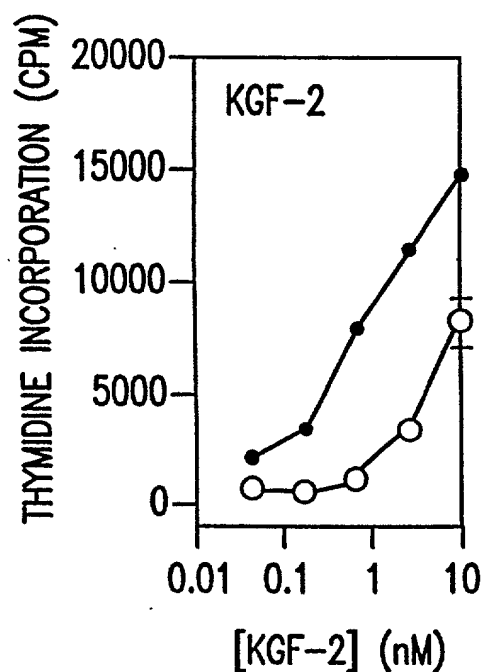


FIG.22A-1

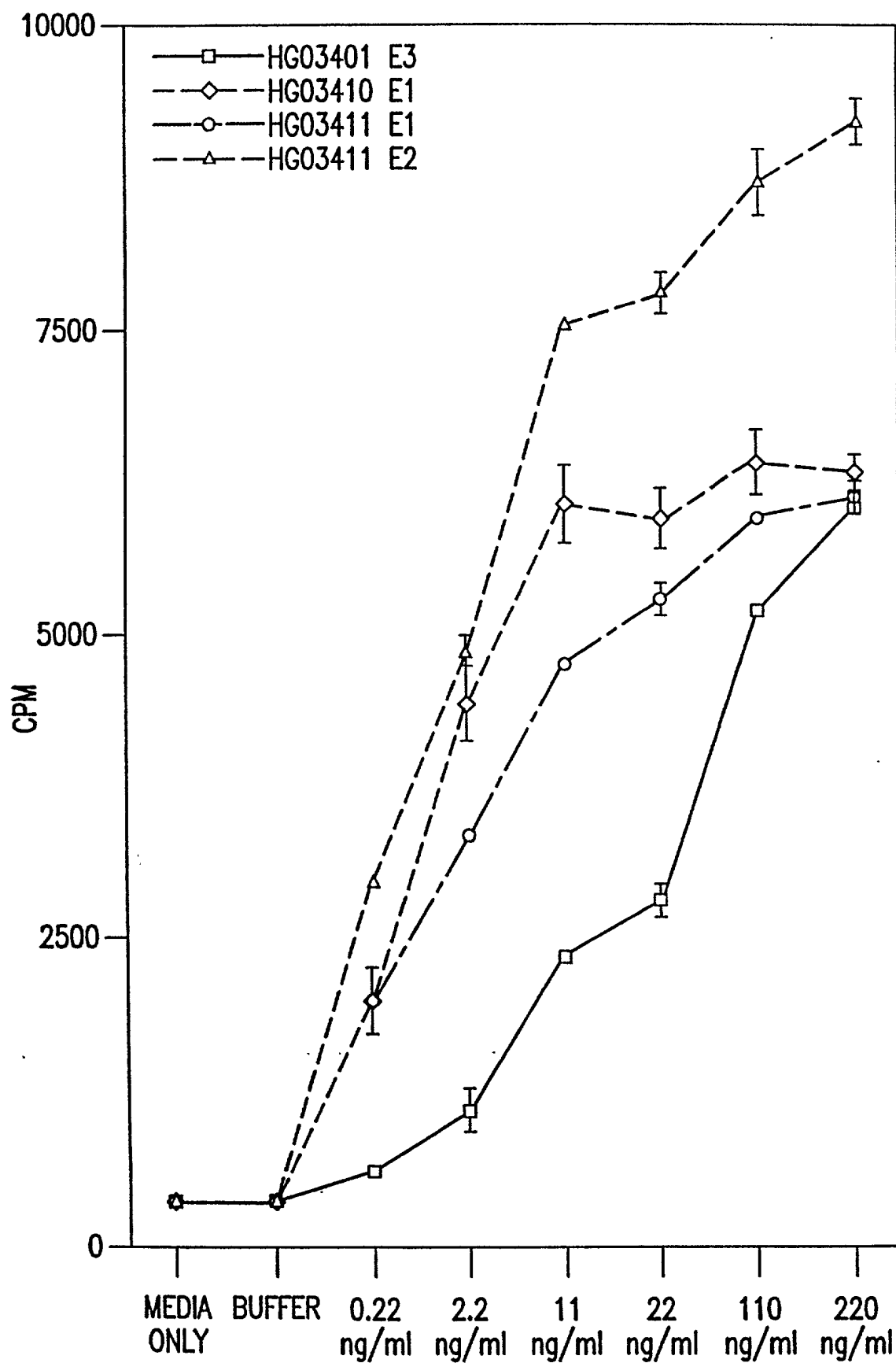


FIG.22B

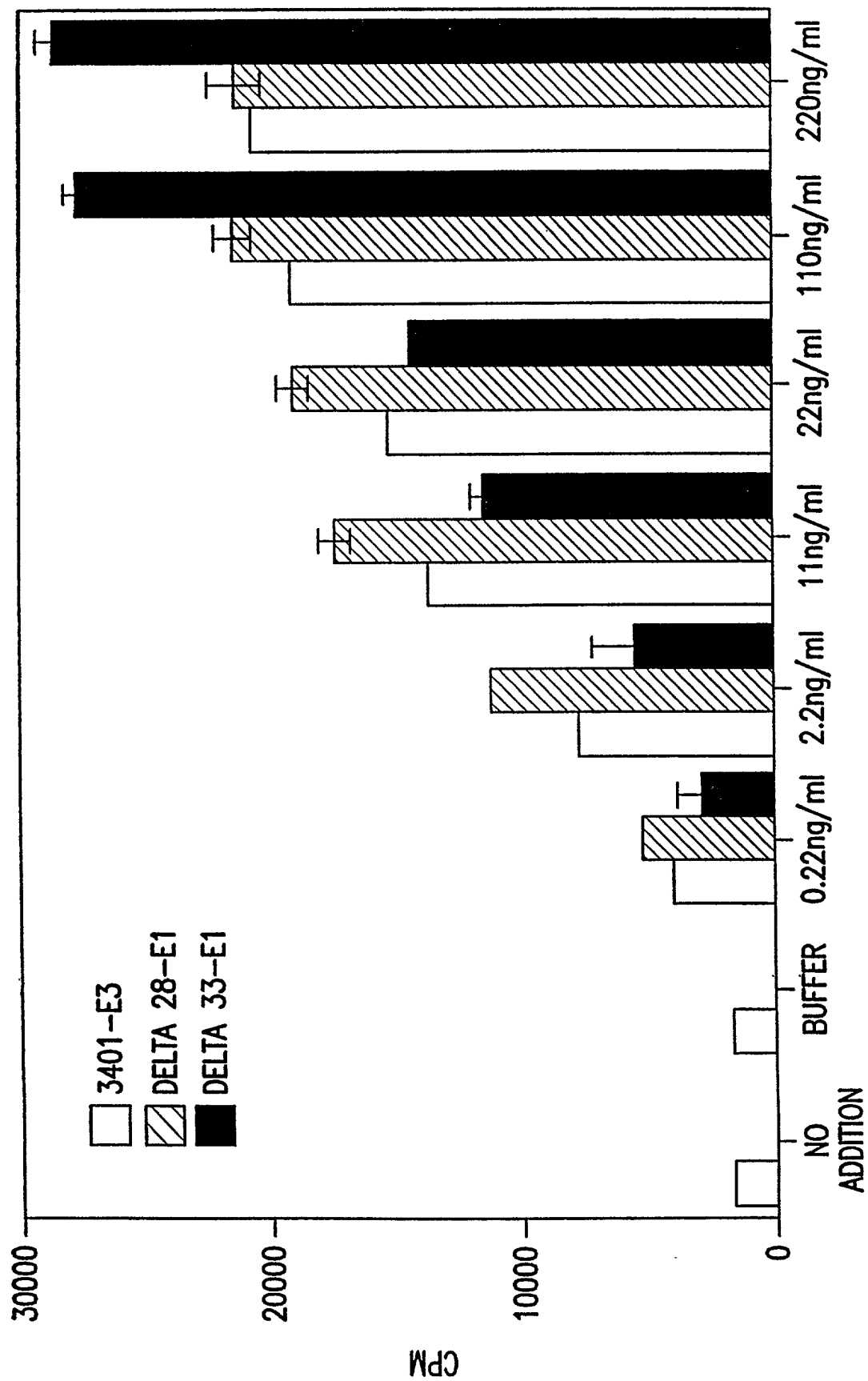


FIG.22C



ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCCTCT 60  
 MetThrCysGlnAlaLeuGlyGlnAspMetValSerProGluAlaThrAsnSerSerSer  
 TCCTCTTTCTCTTCCCGTCTTCCGCTGGTCGTCACGTTGTTCTTACAACCACCTGCAG 120  
 SerSerPheSerSerProSerSerAlaGlyArgHisValArgSerTyrAsnHisLeuGln  
 GGTGACGTTGTTGGCGTAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAA 180  
 GlyAspValArgTrpArgLysLeuPheSerPheThrLysTyrPheLeuLysIleGluLys  
 AACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACA 240  
 AsnGlyLysValSerGlyThrLysLysGluAsnCysProTyrSerIleLeuGluIleThr  
 TCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATG 300  
 SerValGluIleGlyValValAlaValLysAlaIleAsnSerAsnTyrTyrLeuAlaMet  
 AACAGAAGGGGAACTCTATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAGGAG 360  
 AsnLysLysGlyLysLeuTyrGlySerLysGluPheAsnAsnAspCysLysLeuLysGlu  
 AGGATAGAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGG 420  
 ArgIleGluGluAsnGlyTyrAsnThrTyrAlaSerPheAsnTrpGlnHisAsnGlyArg  
 CAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGG 480  
 GlnMetTyrValAlaLeuAsnGlyLysGlyAlaProArgArgGlyGlnLysThrArgArg  
 AAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG 525  
 LysAsnThrSerAlaHisPheLeuProMetValValHisSer \*

FIG.24A

ATGACTTGCCAGGCACTGGGTCAAGACATGGTTTCCCGGAAGCTACCAACAGCTCCAGCTCTAGCTTCA  
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----| 70  
 TACTGAACGGTCCGTGACCCAGTTCTGTACCAAAGGGCCTTCGATGGTTGTCGAGGTGAGATCGAAGT  
 M T C Q A L G Q D M V S P E A T N S S S S S F  
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
 GCAGCCCATCTAGCGCAGGTGTCACGTTGCTCTTACAACCACTTACAGGGTGATGTTGTTGCGCAA  
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----| 140  
 CGTCGGGTAGATCGGTCCAGCAGTGCAAGCGAGAATGTTGGTGAATGTCCCACTACAAGCAACCGGTT  
 S S P S S A G R H V R S Y N H L Q G D V R W R K  
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
 ACTGTTCACTTTACCAAGTACTTCTGAAAATCGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAG  
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----| 210  
 TGACAAGTCGAAATGGTTCATGAAGGACTTTTAGCTTTTTTGGCATTTCAAAGACCCTGGTCTTCTCTC  
 L F S F T K Y F L K I E K N G K V S G T K K E  
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
 AACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACA  
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----| 280  
 TTGACGGGCATGTCGTAGGACCTCTATTGTAGTCATCTTAGCCTCAACAACGGCAGTTTCGGTAATTGT  
 N C P Y S I L E I T S V E I G V V A V K A I N  
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
 GCAACTATTACTTAGCCATGAACAAGAAGGGGAACTCTATGGCTCAAAAGAATTTAACAATGACTGTAA  
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----| 350  
 CGTTGATAATGAATCGGTACTTGTCTTCCCTTTGAGATACCGAGTTTCTTAAATTGTTACTGACATT  
 S N Y Y L A M N K K G K L Y G S K E F N N D C K  
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
 GCTGAAGGAGAGGATAGAGGAAAATGGATAACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGG  
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----| 420  
 CGACTTCCTCTCCTATCTCCTTTTACCTATGTTATGGATACGTAGTAAATTGACCGTCGTATTACCTCC  
 L K E R I E E N G Y N T Y A S F N W Q H N G R  
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
 CAAATGTATGTGGCATTGAATGAAAAGGAGCTCAAGGAGAGGACAGAAAACGGAAGGAAAAACACCT  
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----| 490  
 GTTACATACACCGTAACCTTACCTTTTCTCGAGGTTCTCTCTCTTGTGCTTCTTTTGTGGA  
 Q M Y V A L N G K G A P R R G Q K T R R K N T  
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|  
 CTGCTCACTTTCTTCCAATGGTGGTACACTCATAG  
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----| 525  
 GACGAGTGAAAGAAGGTTACCACCATGTGAGTATC  
 S A H F L P M V V H S  
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

FIG.24B



2040 212501

ATGACCTGCCAGGCTCTGGGTGAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC  
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCACGTTTCGTTCTTACAACCAC  
CTGCAGGGTGACGTTTCGTTGGCGTAAACTGTTCTTTTACCAAATACTTCCTGAAA  
ATCGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCCGTACAGCATC  
CTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAAACAGCAAC  
TATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAGAATTAAACAAT  
GACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTT  
AACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCA  
AGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTG  
GTACACTCATAG

MTCQALGQDMVSPEATNSSSSSFSSPSAGRHVRSYNHLQGDVWRKLFSTKYFLKIE  
KNGKVSQTKKENCYPYSILEITSVEIGVVAVKAINSNYLAMNKKGKLYGSKEFNNDCKL  
KERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

FIG.25

ATGGCTGGTCGTCACGTTTCGTTCTTACAACCACCTGCAGGGTGACGTTTCGTTGGCGT  
AAACTGTTCTCTTTTACCAAATACTTCCTGAAAATCGAAAAAACGGTAAAGTTTCT  
GGGACCAAGAAGGAGAACTGCCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATC  
GGAGTTGTTGCCGTCAAAGCCATTAAACAGCAACTATTACTTAGCCATGAACAAGAAG  
GGGAAACTCTATGGCTCAAAGAATTAAACAATGACTGTAAGCTGAAGGAGAGGATA  
GAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAA  
ATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGG  
AAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MAGRHVRSYNHLQGDVWRKLFSTKYFLKIEKNGKVSQTKKENCYPYSILEITSVEIGV  
VAVKAINSNYLAMNKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVA  
LNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

FIG.26

ATGGTTCGTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAA  
AACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCCGTACAGCATCCTGGAGATA  
ACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAAACAGCAACTATTACTTA  
GCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAGAATTTAACAATGACTGTAAG  
CTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAG  
CATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGA  
CAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCA  
TAG

MVRWRKLFSTKYFLKIEKNGKVSgtKKENCpysILEITSVEIGVVAVKAINSnyyLAM  
NKKGKLYGSKEFNNDCKLKERIEENGyNTYASFNWQHNGRQMYVALNGKGAPRRGQKTR  
RKNTSAHFLPMVVHS.

FIG.27

ATGGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCCGTACAGCAT  
CCTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAAACAGCA  
ACTATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAGAATTTAAC  
AATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATC  
ATTTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAG  
CTCCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCA  
ATGGTGGTACACTCATAG

MEKNGKVSgtKKENCpysILEITSVEIGVVAVKAINSnyyLAMNKKGKLYGSKEFNND  
CLKERIEENGyNTYASFNWQHNGRQMYVALNGKGAPRRGQKTRRKNTSAHFLPMVVH  
S.

FIG.28

Variable	Mean	SD	Min	Max
Age	45.2	12.5	25	65
Gender	0.5	0.5	0	1
Marital status	0.7	0.5	0	1
Education	12.5	2.5	9	16
Income	35000	15000	10000	70000
Health status	0.8	0.4	0	1
Exercise frequency	2.5	1.5	0	5
Stress level	4.5	1.5	1	7
Sleep quality	3.5	1.5	1	5
Diet quality	4.0	1.5	1	5
Alcohol consumption	1.5	1.5	0	5
Tobacco use	0.5	0.5	0	1
Family size	2.5	1.5	1	5
Work hours	40	10	20	60
Commuting time	30	15	10	60
Childcare costs	500	200	0	1000
Health insurance	0.9	0.3	0	1
Access to healthcare	0.8	0.4	0	1
Healthcare costs	1000	500	0	2000
Overall health score	75	10	50	100

FIG. 29

MVKAINSNYYLAMNKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMY  
VALNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

FIG. 30

MGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKT  
RRKNTSAHFLPMVVHS.

FIG. 31

ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC  
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTCTTACAACCAC  
CTGCAGGGTGACGTTCTGTTGGCGTAACTGTTCTCTTTCACCAAATACTTCCTGAAA  
ATCGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATC  
CTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAAC  
TATTACTTAGCCATGAACAAGAAGGGGAACTCTATGGCTCAAAGAATTTAACAAT  
GACTGTAAGCTGAAG

MTCQALGQDMVSPEATNSSSSSFSSPSSAGRHVRSYNHLQGDVRWRKLFSTKYFLKIE  
KNGKVSGETTKENCPYSILEITSVEIGVVAVKAINSNYLAMNKKGKLYGSKEFNNDCKL  
K

FIG.32

ATGGCTGGTCGTCACGTTCTTACAACCACCTGCAGGGTGACGTTCTGTTGGCGT  
AACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAAACGGTAAAGTTTCT  
GGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATC  
GGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAG  
GGGAACTCTATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAG

MAGRHVRSYNHLQGDVRWRKLFSTKYFLKIEKNGKVSGETTKENCPYSILEITSVEIGV  
VAVKAINSNYLAMNKKGKLYGSKEFNNDCKLK

FIG.33

C-37 To Ser

ATGACCTCTCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC  
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTGTTCTTACAACCAC  
CTGCAGGGTGACGTTGTTGGCGTAACTGTTCTCTTTCACCAAATACTTCCTGAAA  
ATCGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCCGTACAGCATC  
CTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAAACAGCAAC  
TATTACTTAGCCATGAACAAGAAGGGGAACTCTATGGCTCAAAGAATTTAACAAT  
GACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTT  
AACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCA  
AGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTG  
GTACACTCATAG

FIG.34

C-106 To Ser

ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC  
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTGTTCTTACAACCAC  
CTGCAGGGTGACGTTGTTGGCGTAACTGTTCTCTTTCACCAAATACTTCCTGAAA  
ATCGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTCTCCGTACAGCATC  
CTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAAACAGCAAC  
TATTACTTAGCCATGAACAAGAAGGGGAACTCTATGGCTCAAAGAATTTAACAAT  
GACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTT  
AACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCA  
AGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTG  
GTACACTCATAG

FIG.35

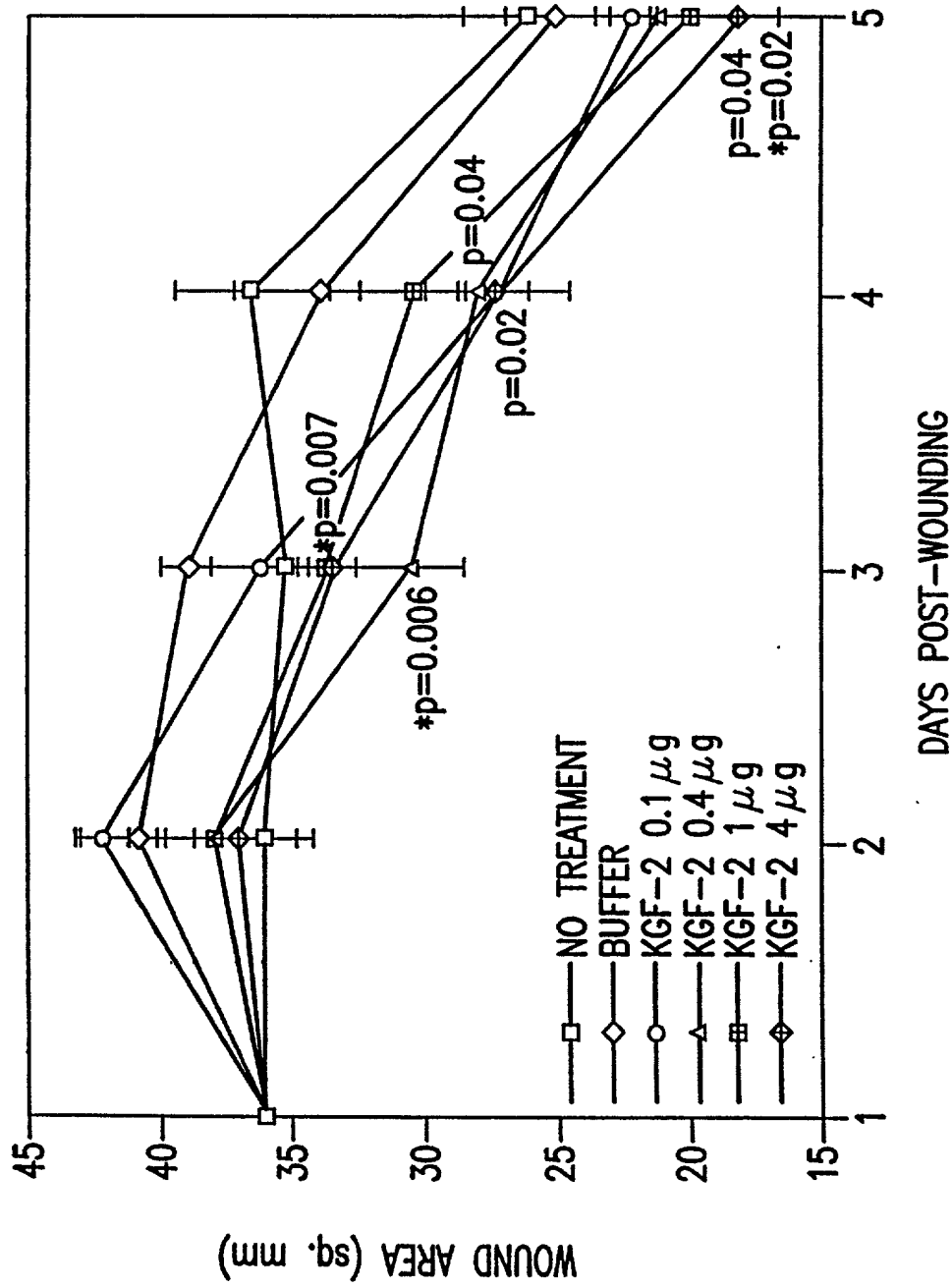


FIG.36

EFFECT OF KGF-2  $\Delta 33$  ON NORMAL WOUND HEALING RAT MODEL

TREATMENT GROUPS	WOUND SIZE (mm)	% WOUND CLOSURE	HISTOLOGICAL SCORE	RE-EPITH. ( $\mu m$ )	BrdU SCORE
NO TREATMENT	25.9 $\pm$ 2.5	58.8 $\pm$ 3.7	6.8 $\pm$ 0.2	1142 $\pm$ 141	3.8 $\pm$ 0.4
BUFFER	25.1 $\pm$ 1.7	60.2 $\pm$ 2.6	6.4 $\pm$ 0.2	923 $\pm$ 61	5.0 $\pm$ 0.4
KGF-2/ $\Delta 33$ (0.1 $\mu g$ )	22.0 $\pm$ 0.9	65 $\pm$ 1.4	6.8 $\pm$ 0.2	1275 $\pm$ 148	4.6 $\pm$ 0.7
KGF-2/ $\Delta 33$ (0.4 $\mu g$ )	21.1 $\pm$ 1.4	68.4 $\pm$ 2.4	8.0 $\pm$ 0.5 p=0.0445*	1310 $\pm$ 182	4.2 $\pm$ 0.7
KGF-2/ $\Delta 33$ (1.0 $\mu g$ )	19.9 $\pm$ 1.5	66.2 $\pm$ 2.1	8.4 $\pm$ 0.4 p=0.0159* p=0.0053†	1389 $\pm$ 115 p=0.0074†	3.3 $\pm$ 0.25 p=0.0217†
KGF-2/ $\Delta 33$ (4.0 $\mu g$ )	18.1 $\pm$ 1.6 p=0.0398* p=0.0200†	71.2 $\pm$ 2.6 p=0.0367* p=0.0217†	8.5 $\pm$ 0.3 p=0.0047* p=0.0445†	1220 $\pm$ 89 p=0.0254†	5.3 $\pm$ 0.9

FIG.37

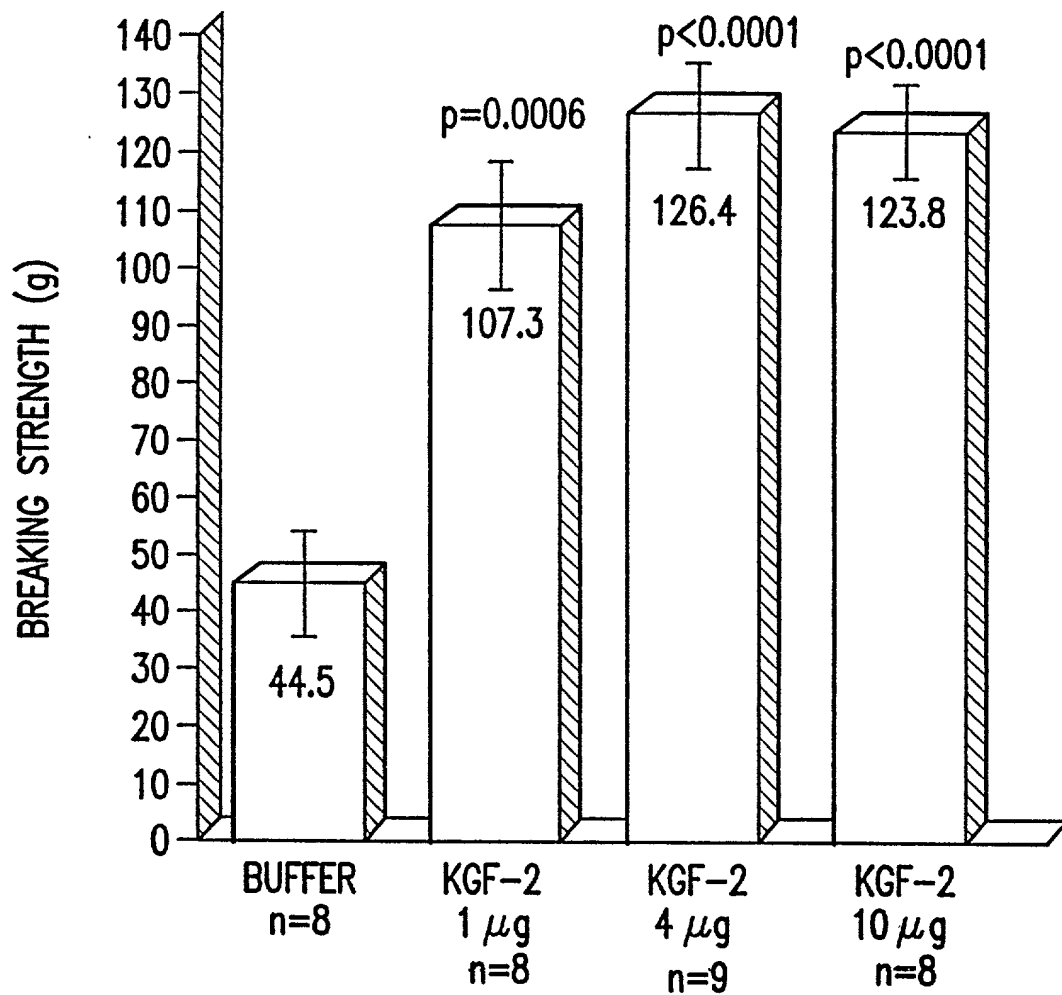


FIG.38



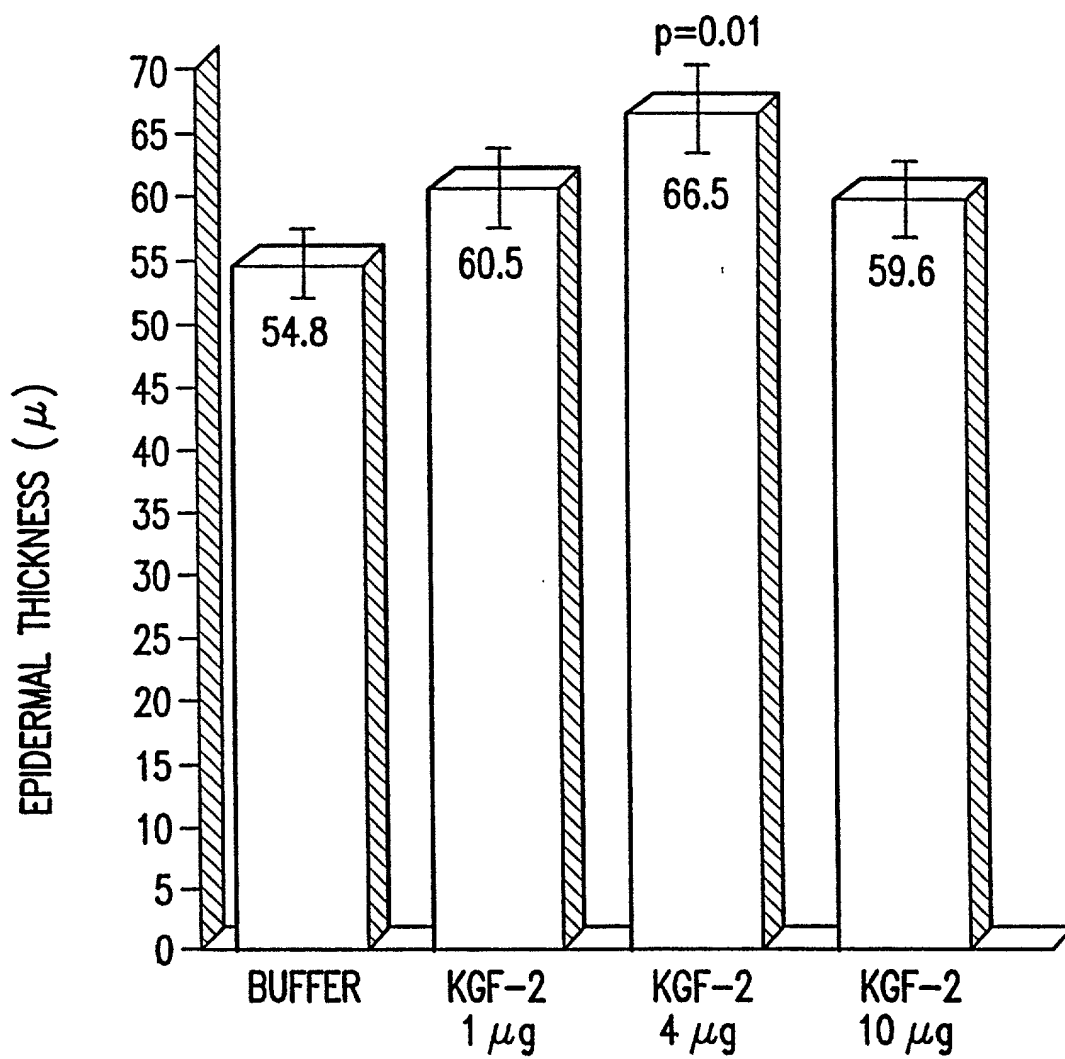


FIG.39

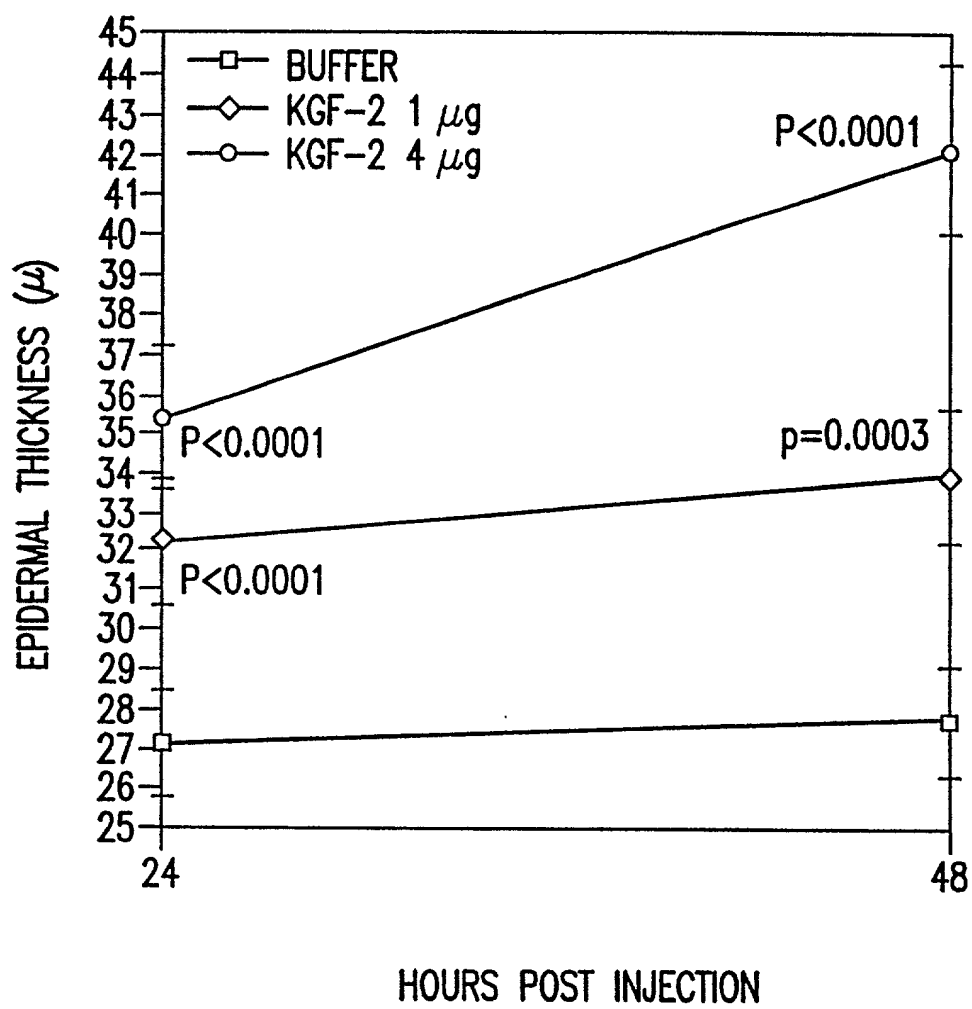


FIG.40

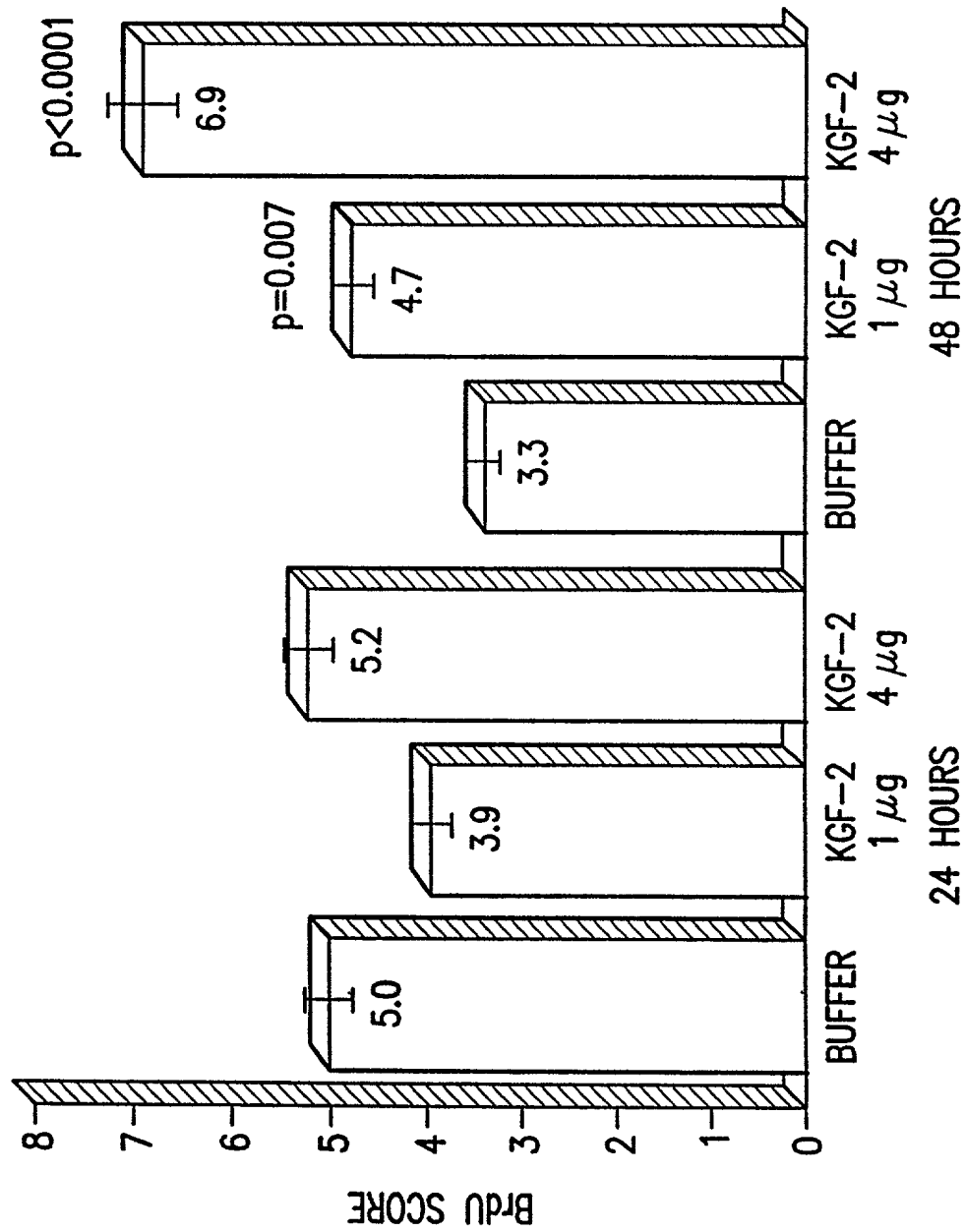


FIG.41

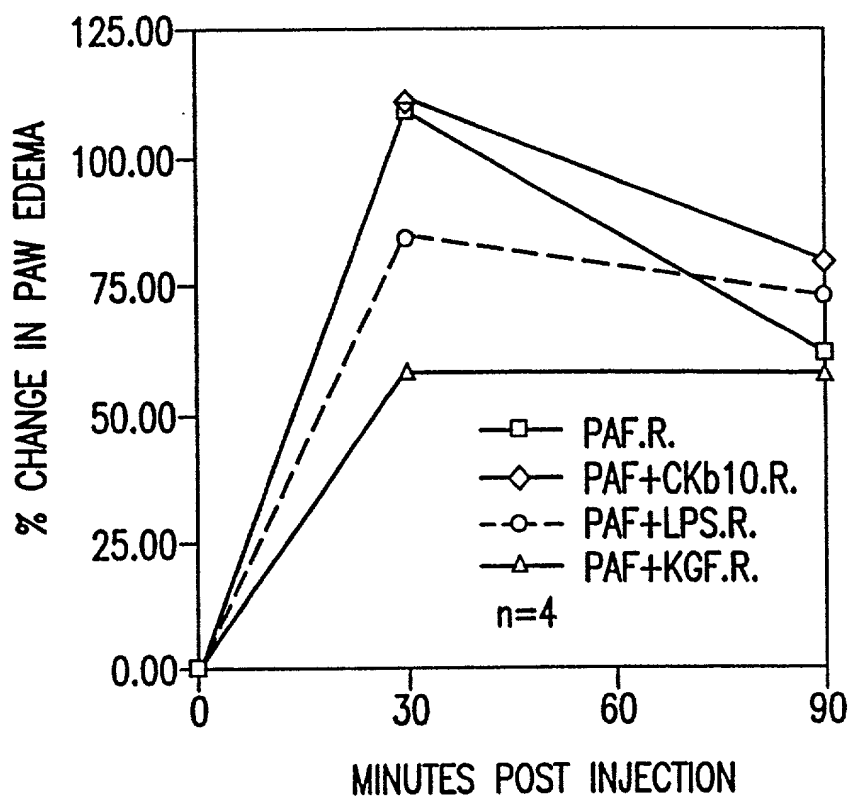


FIG.42A

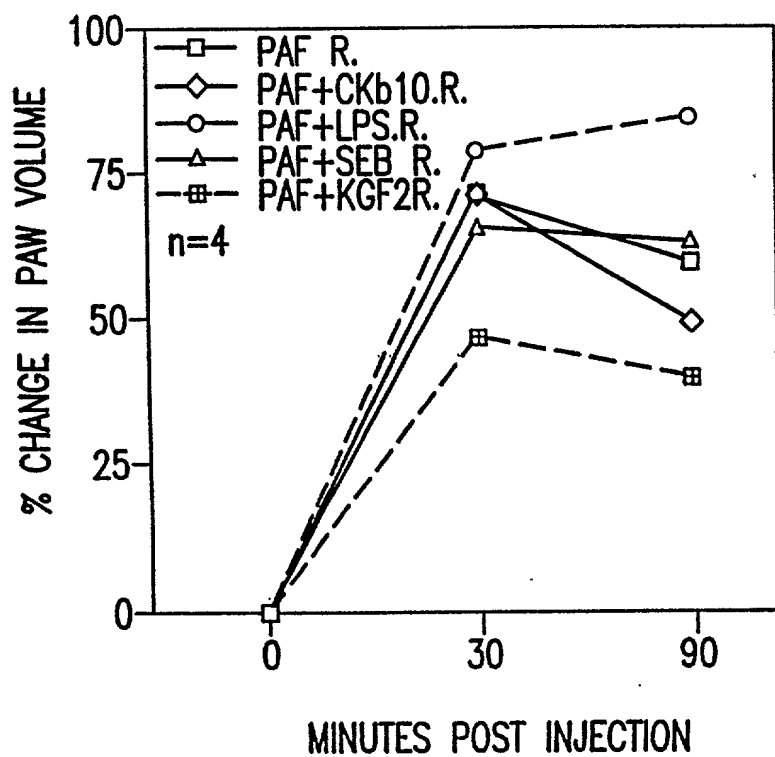


FIG.42B

# EFFECT OF KGF-2 $\Delta 33$ ON PAF-INDUCED PAW EDEMA IN LEWIS RATS

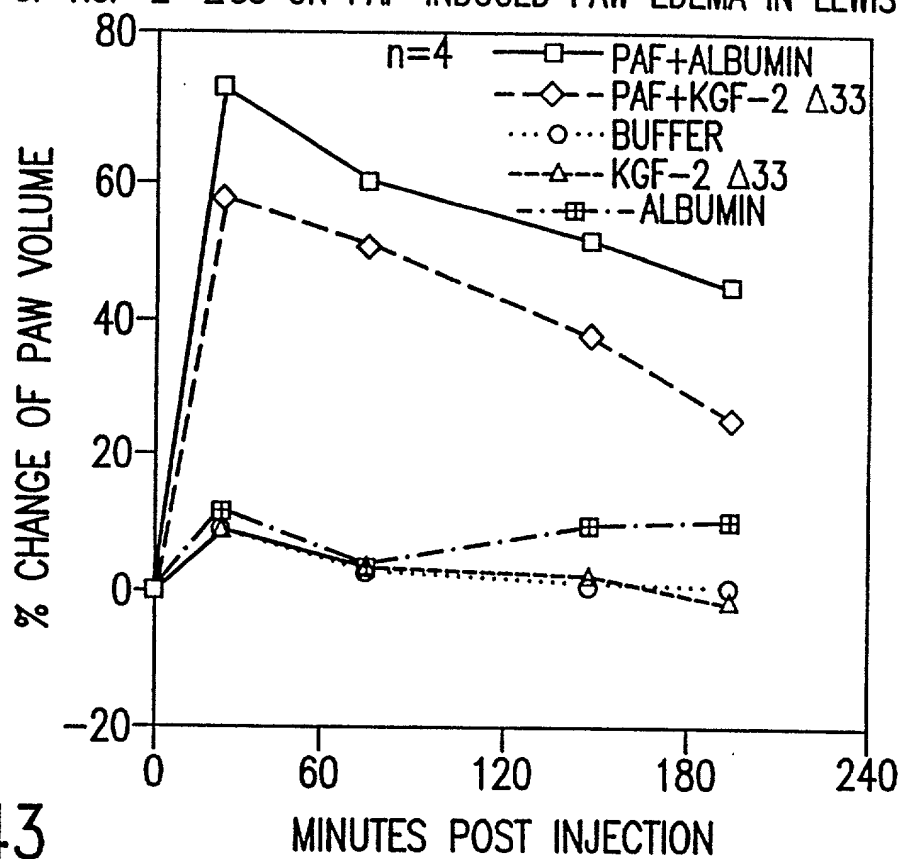


FIG.43

# EFFECT OF KGF-2 $\Delta 33$ ON SURVIVAL OF WHOLE BODY IRRADIATED Balb/c MICE

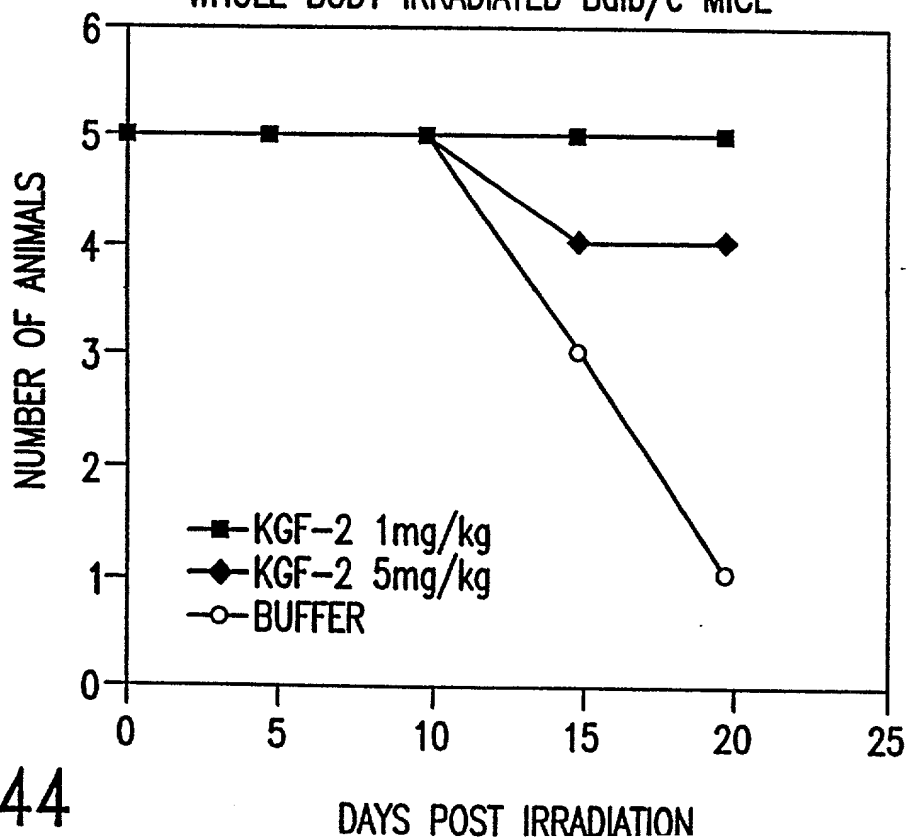


FIG.44

# EFFECT OF KGF-2 $\Delta 33$ ON BODY WEIGHT OF IRRADIATED MICE

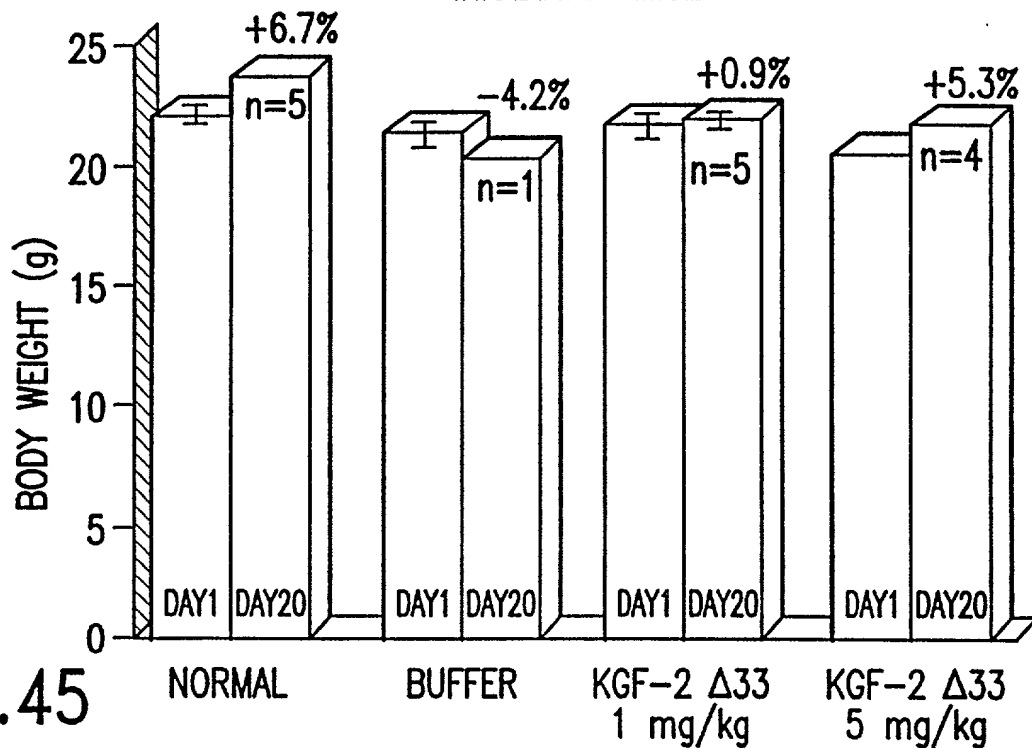
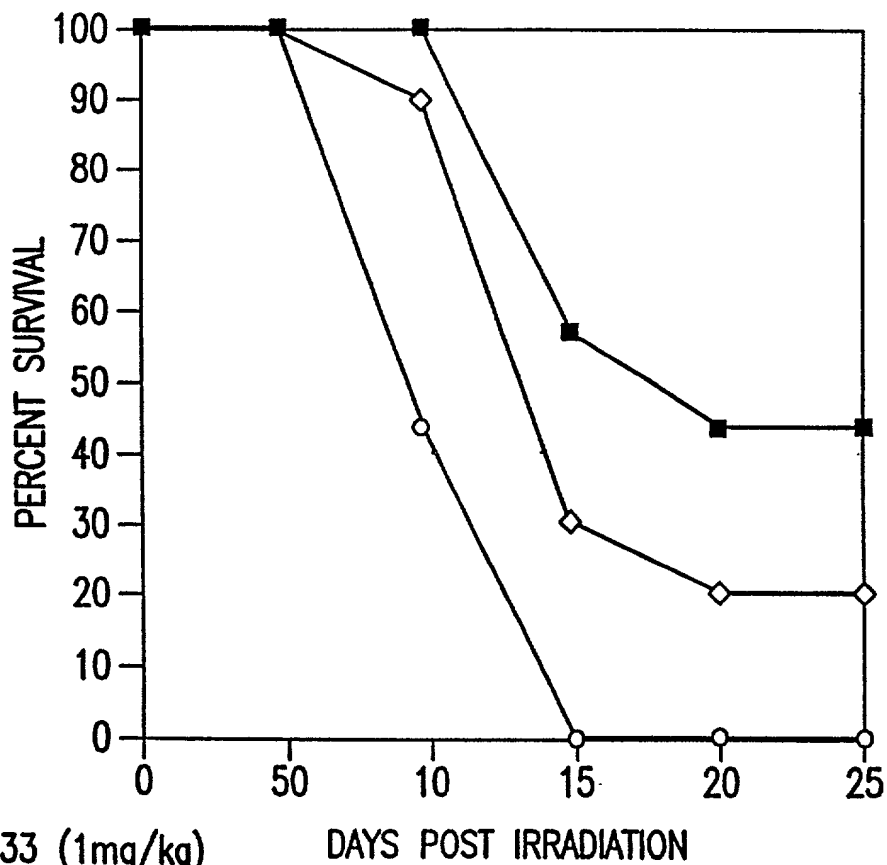


FIG.45



◇ KGF-2  $\Delta 33$  (1mg/kg)  
 ■ KGF-2  $\Delta 33$  (5mg/kg)  
 ○ BUFFER

DAYS POST IRRADIATION

FIG. 46

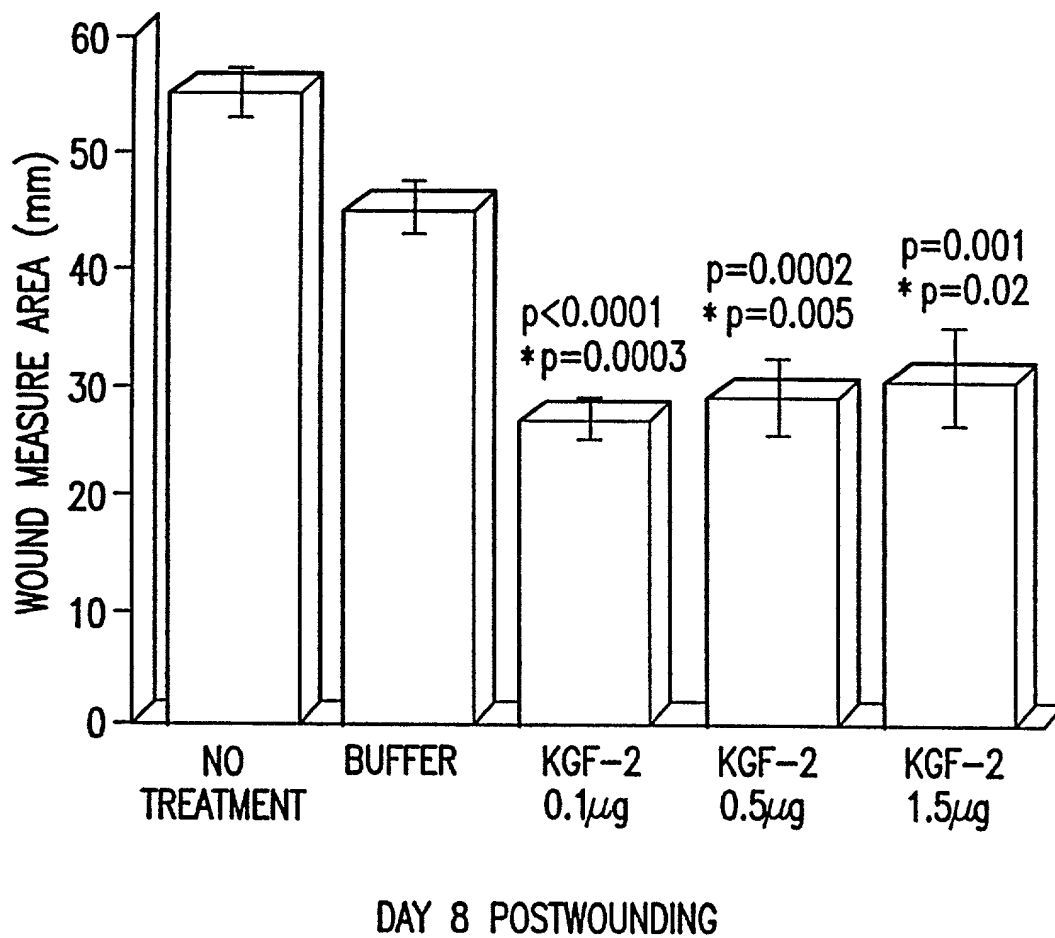


FIG.47

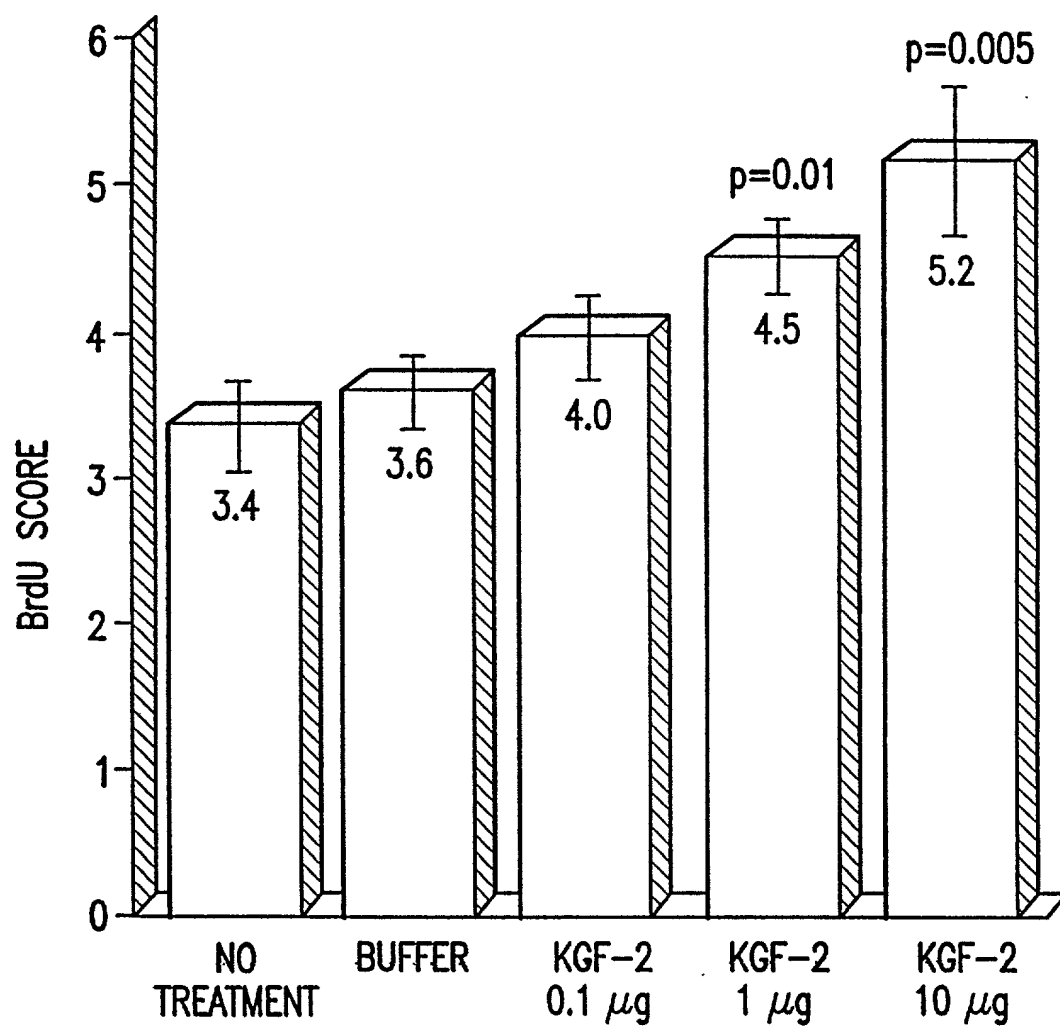


FIG.48



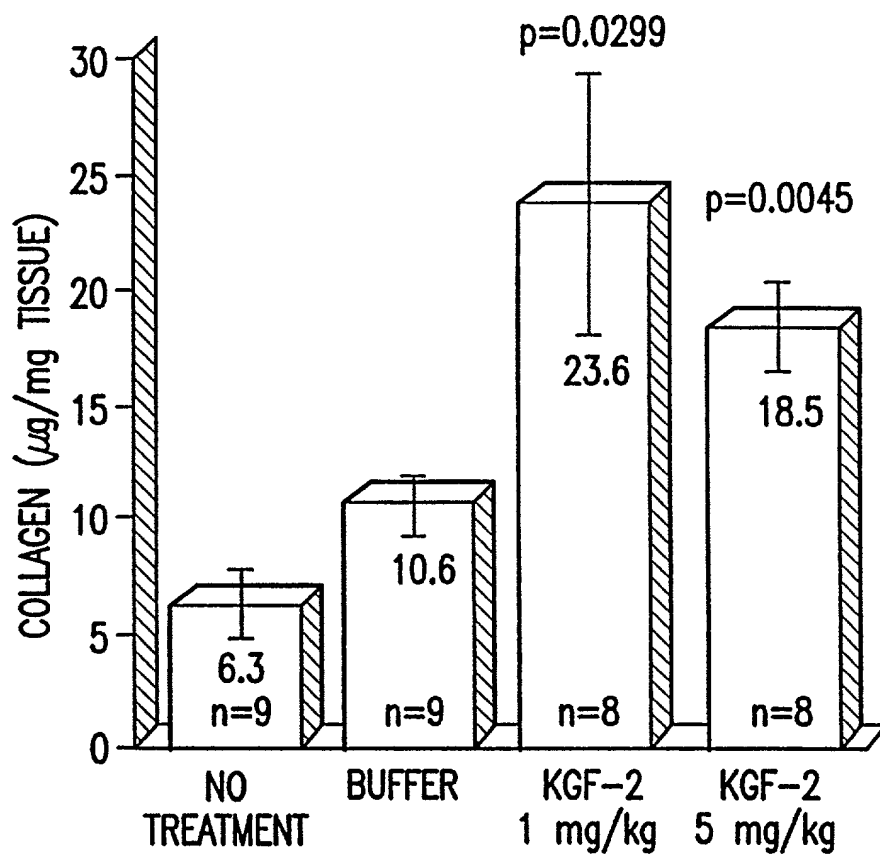


FIG.49

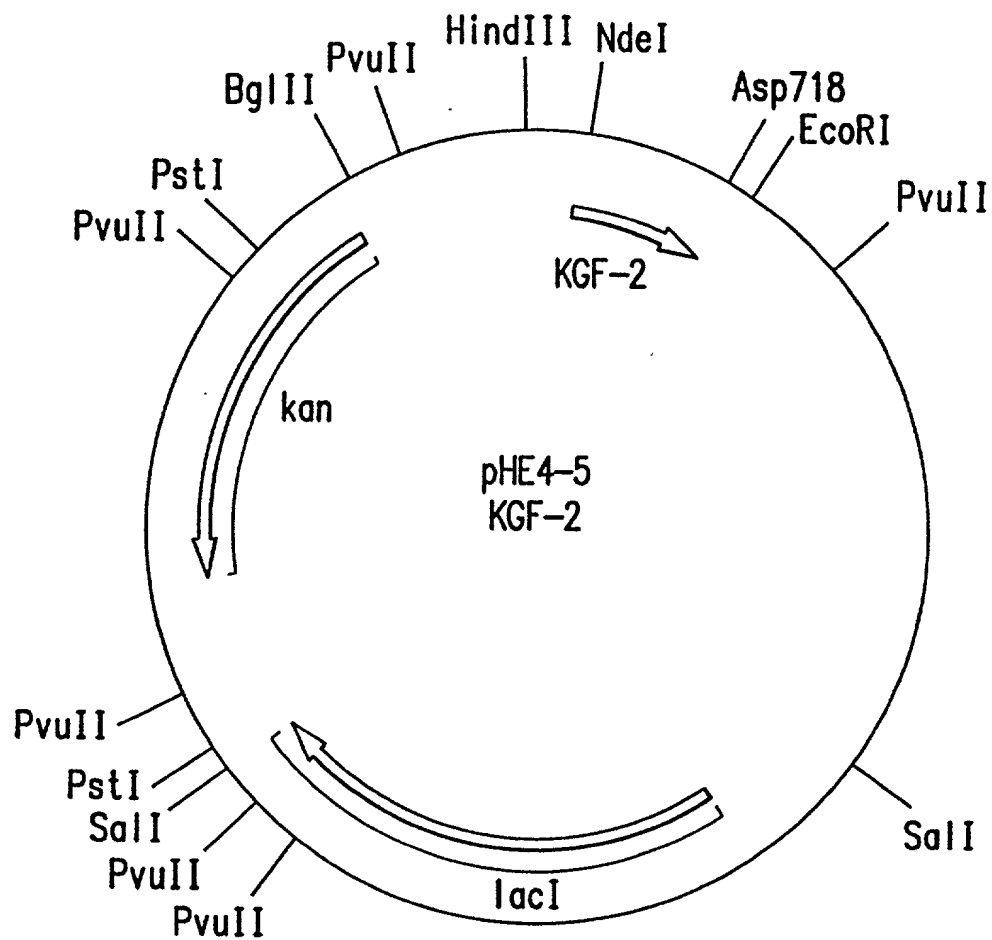


FIG. 50

1      AAGCTTAAAAAACTGCAAAAATAGT <sup>-35</sup> T T G A C T <sup>Operator 1</sup> (TGTGAGCGGATAACAAT)

50      <sup>-10</sup> TAAGAT GTACCCA <sup>Operator 2</sup> (ATTGTGAGCGGATAACAAT) TTCACACATTAA

94      <sup>S/D</sup> AGAGGAGAAATTA CATATG

FIG. 51

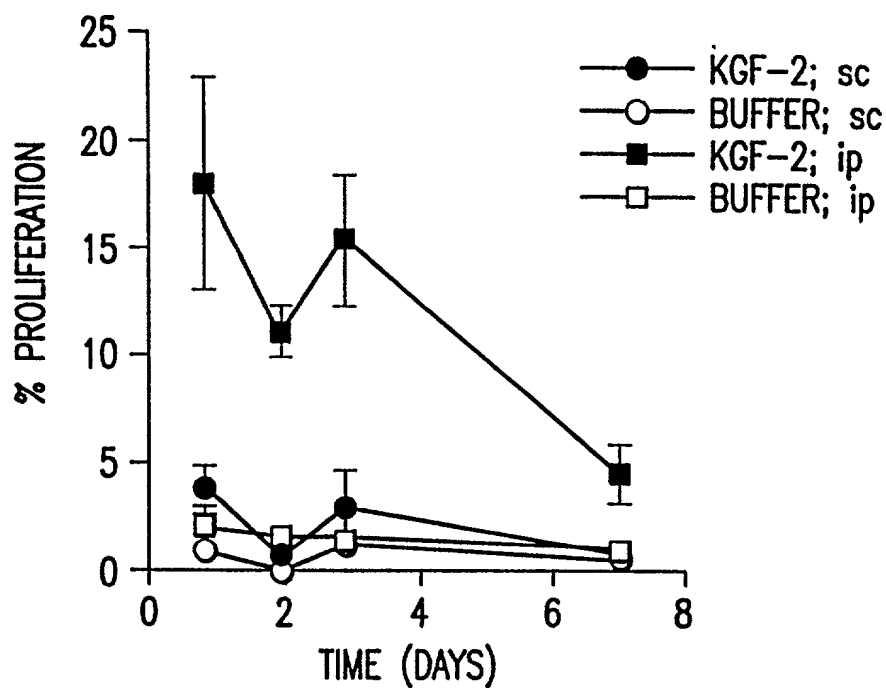


FIG. 52

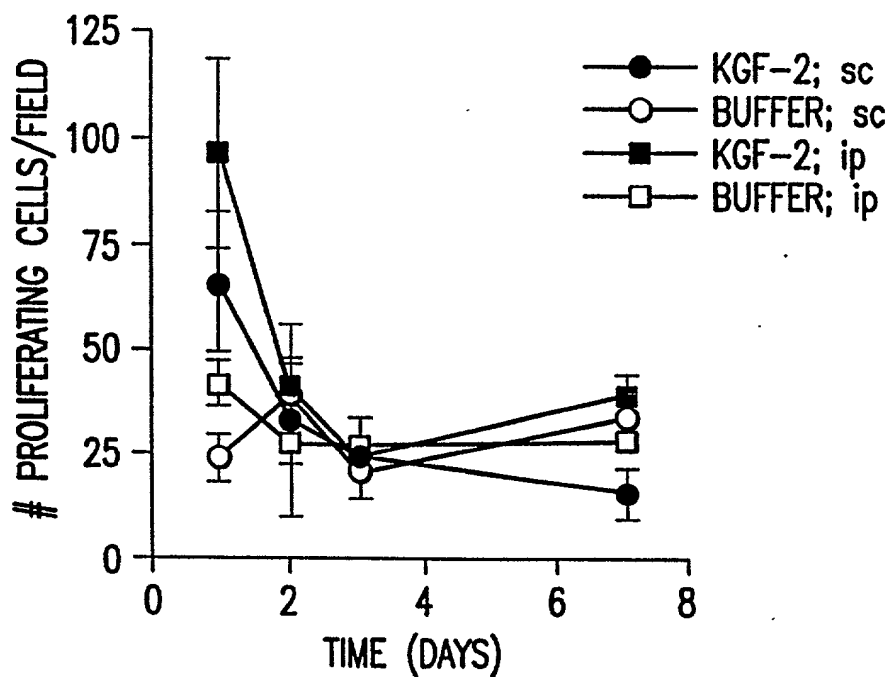


FIG. 53

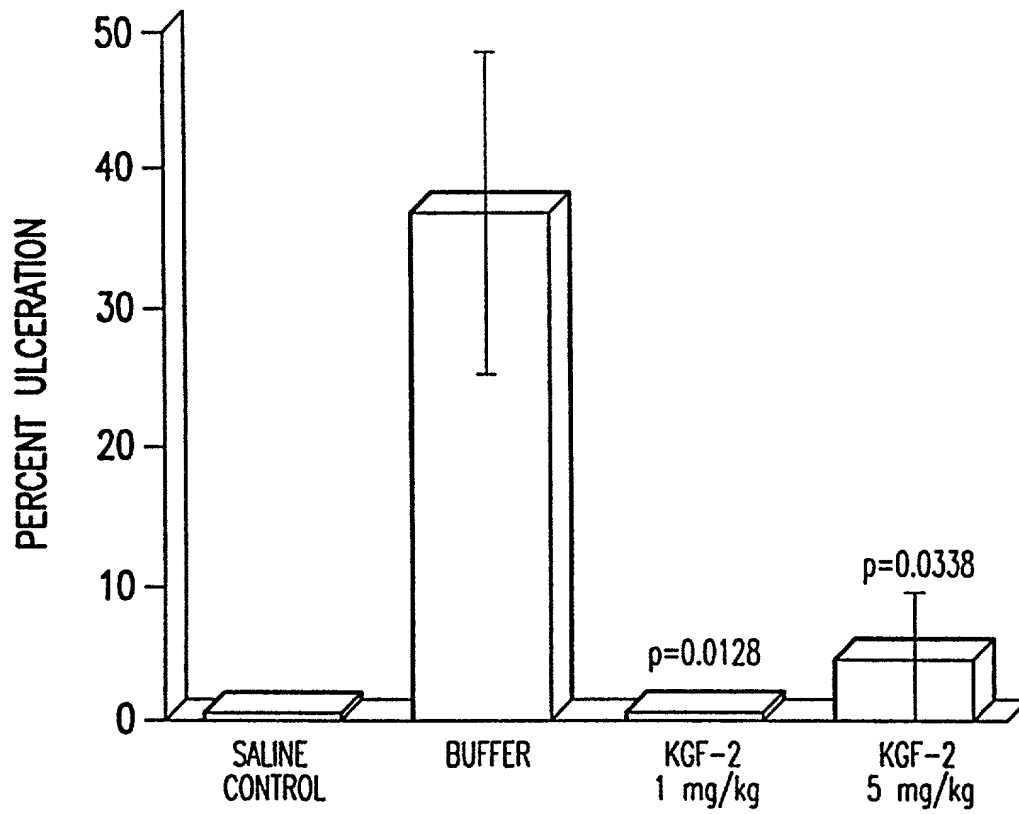


FIG. 54

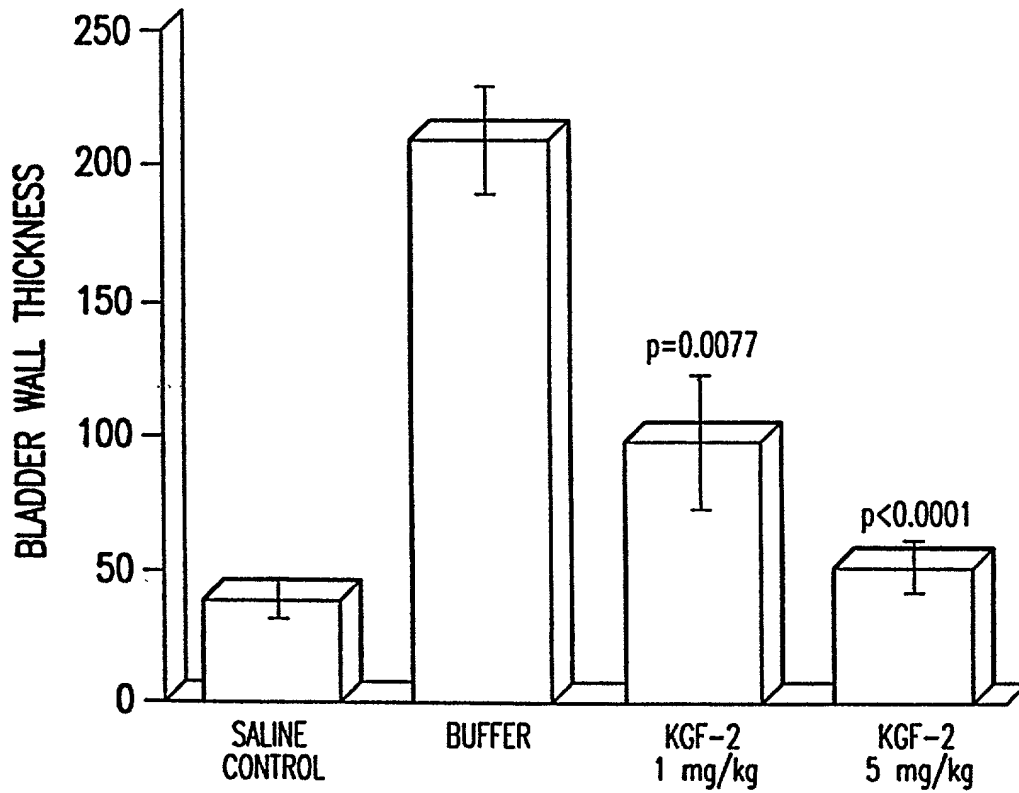


FIG. 55

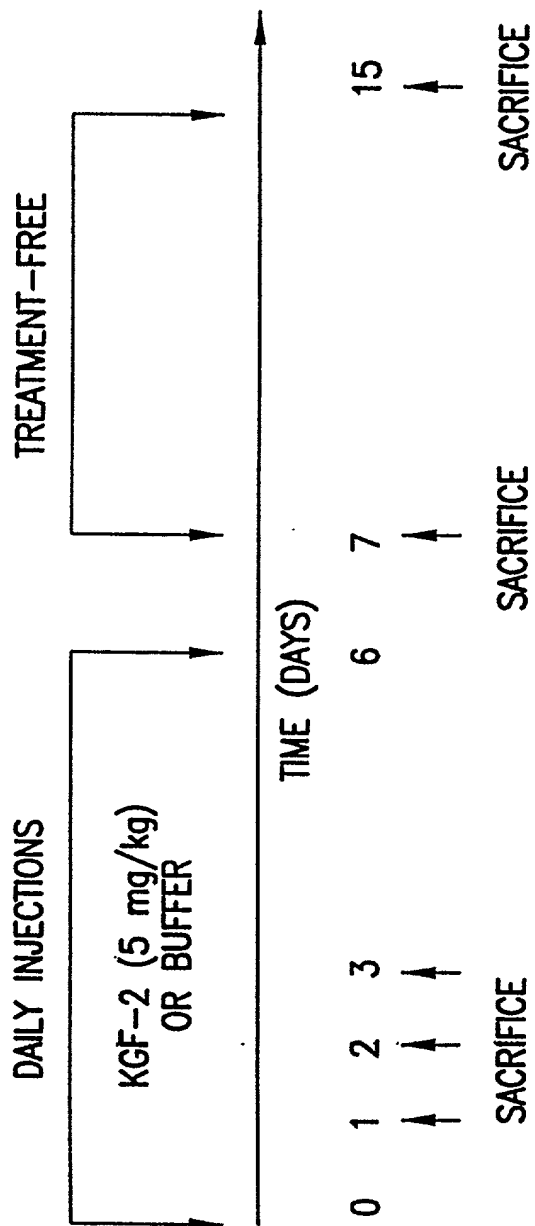


FIG. 56

PROLIFERATION OF HEPATOCYTES FOLLOWING SYSTEMIC ADMINISTRATION OF KGF-2

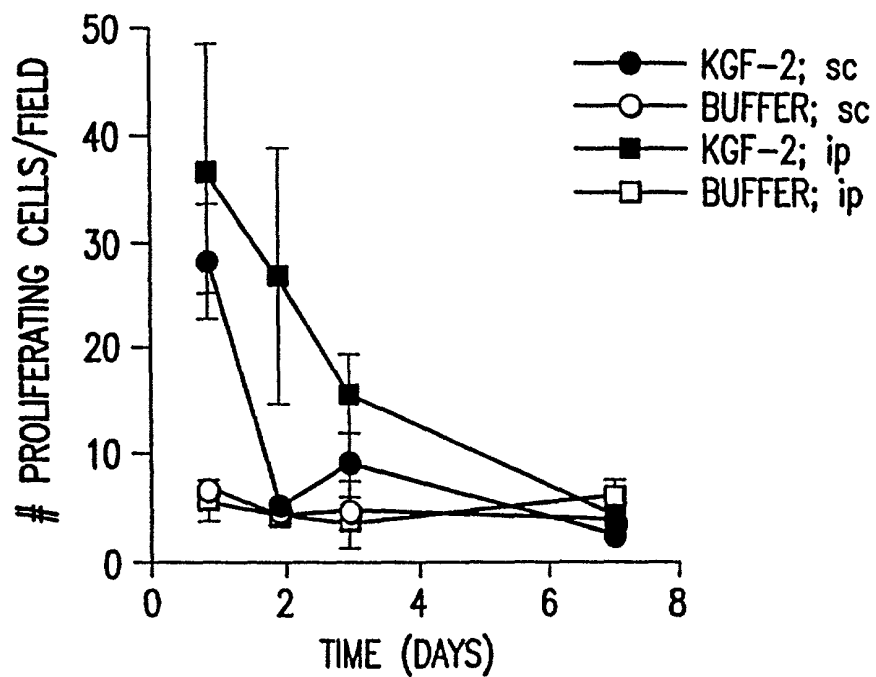


FIG. 57

PROLIFERATION OF PANCREATIC CELLS FOLLOWING SYSTEMIC ADMINISTRATION OF KGF-2

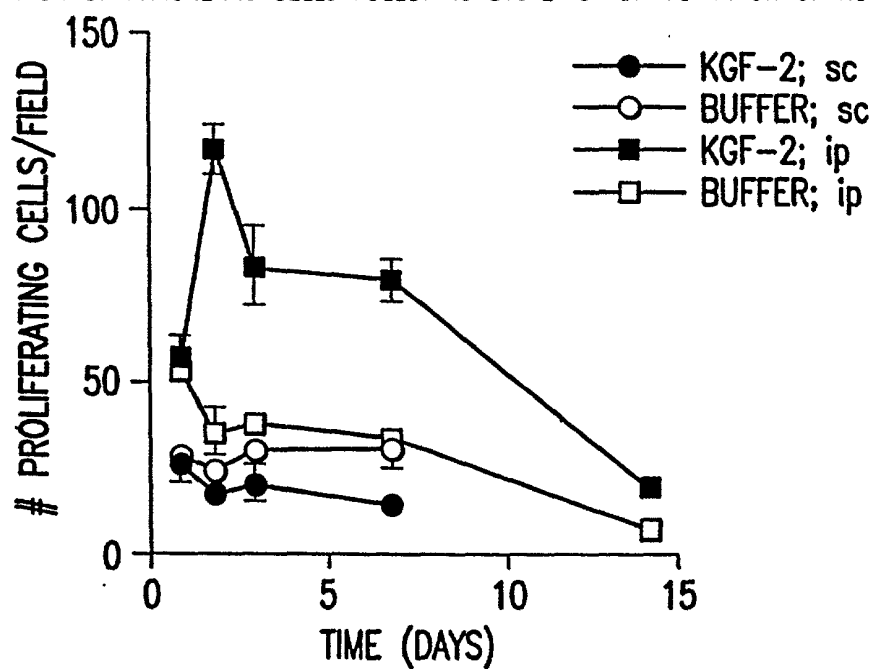


FIG. 58

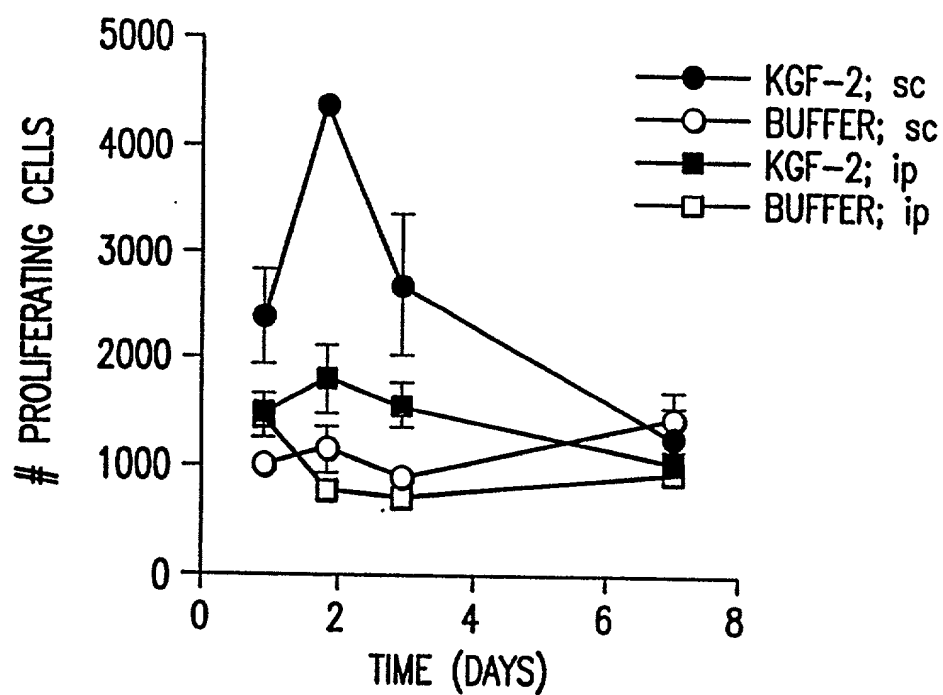


FIG. 59

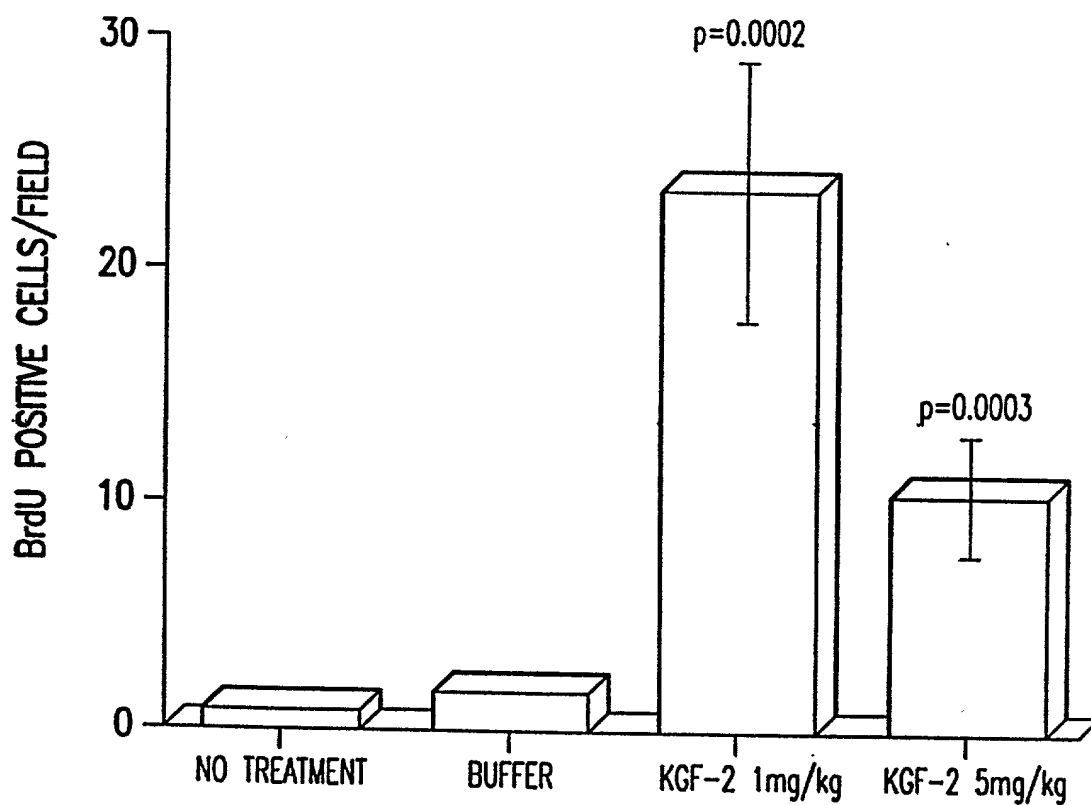


FIG. 60